

Access DB# 83111

# SEARCH REQUEST FORM

Scientific and Technical Information Center

*CRF*

Requester's Full Name: M.A. WALICKA Examiner #: 7820 Date: 11/21/02  
 Art Unit: 1652 Phone Number 305-7270 Serial Number: 151136 311  
 Mail Box and Bldg Room Location: 16306 Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*  
 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract

Title of Invention: Monitor method for measuring protein phospho at

Inventors (please provide full names): MAGWARA

Earliest Priority Filing Date: 09/02/1998

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please search SEQ ID NO:1 Seq is OK  
 SEQ ID NO:2

Thank you in advance.

Edward H. ...  
 Technical Info. Specialist  
 STIC/Biotech  
 CMI 6B02 Tel: 305-9203

*Wolicki*

AA  
 1-23  
 2-23

## STAFF USE ONLY

Staff Use Only	Type of Search	Vendors and cost where applicable
Searcher <u>11/21/03</u>	NA Sequence (#) <u>2</u>	STN
Searcher Phone # <u>11/21/03</u>	AA Sequence (#)	Dialog
Searcher Location	Structure (#)	Questel Orbit
Date Searcher Picked Up <u>11/21/03</u>	Bibliographic	Dr Link
Date Completed <u>11/21/03</u>	Litigation	LexisNexis
Searcher Prep & Review Time	Fulltext	Sequence Systems <u>pr</u>
Clencal Prep Time	Patent Family	WWW Internet
Online Time	Other	Other (specify)















RT "Human CREM gene: evolutionary conservation, chromosomal localization,  
 RI and inducibility of the transcript";  
 RC Cell Growth Differ. 4:931-937(1993).  
 CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY.

CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY.  
 CR EMBL: S68271; AAC60616.2; -;  
 DR InterPro: IPR001630; Leuzip\_CREB.  
 DR InterPro: IPR002112; Leuzip\_Jun.  
 DR InterPro: IPR003102; PKID.  
 DR InterPro: IPR004827; TF\_BZIP.  
 DR Pfam: PF00170; BZIP; 1.  
 DR Pfam: PF02173; PKID; 1.  
 DR PRINTS: PR00041; LEUZIP\_CREB.  
 DR PRINTS: PR00043; LEUZIP\_JUN.  
 DR SMART: SM00338; BRLZ; 1.  
 DR PROSITE: PS00036; BZIP\_BASIC; 1.  
 KW DNA-binding: Nuclear protein.  
 SQ SEQUENCE 232 AA; 25817 MW; PEP091PECC797A36 CRC64;

Query Match 80.2%; Score 89; DB 4; Length 332;  
 Best Local Similarity 94.7%; Pred. No. 3.8e-06;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRKPSYRKILNLSDD 22  
 IILSRKPSYRKILNLSDD 131

Search completed: January 2, 2003, 12:30:43  
 Job time : 26.5 secs

Gapdpe version 5.1.3  
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EM protein protein search, using sw model

Jan 03 January 20 2003 12:26:31 Search time: 7 seconds  
(without alignments)  
146,279 Million cell updates/sec

Hit(s) 95 69 796 417 1  
Protein source: 111  
Sequence: 1 ISSUES:SPRDSYKRLINDLSST 23

Scoring table: RZSDM62  
Gapdpe 10.0, Gapext 0.5

Searches: 112862 seqs, 414762B residues

Total number of hits satisfying chosen parameters: 112862

Minimum hit seq length: 9

Maximum hit seq length: 200000000

Post processing: Minimum Match 0.4

Maximum Match 100%

Listed first 45 summaries

Database: SwissProt 40; \*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Prod. No.	Score	Match	Length	DB	Description
1	93	85.8	426	1	QREB_BOVIN
2	93	83.8	441	1	QREB_HUMAN
3	93	83.8	441	1	QREB_MOUSE
4	93	83.8	441	1	QREB_RAT
5	89	80.2	229	1	QREB_HUMAN
6	89	80.2	441	1	QREB_MOUSE
7	89	80.2	441	1	QREB_RAT
8	89	80.2	441	1	QREB_CANEA
9	75	67.6	217	1	QREB_HYDRA
10	75	67.6	249	1	QREB_CHLOR
11	75	67.6	269	1	QREB_MOUSE
12	75	67.6	271	1	QREB_HUMAN
13	47	42.4	666	1	QREB_MOUSE
14	47	42.4	1100	1	QREB_MOUSE
15	47	42.4	1299	1	QREB_MOUSE
16	45	40.5	593	1	QREB_HUMAN
17	45	40.5	692	1	QREB_MOUSE
18	45	40.5	702	1	QREB_MOUSE
19	44	39.4	437	1	QREB_MOUSE
20	44	39.4	454	1	QREB_MOUSE
21	44	39.4	406	1	QREB_MOUSE
22	44	39.4	711	1	QREB_MOUSE
23	44	39.4	908	1	QREB_MOUSE
24	44	39.4	1124	1	QREB_MOUSE
25	44	39.4	1142	1	QREB_MOUSE
26	44	39.4	1180	1	QREB_MOUSE
27	44	39.4	1187	1	QREB_MOUSE
28	44	39.4	1217	1	QREB_MOUSE
29	44	39.4	1217	1	QREB_MOUSE
30	44	39.4	1217	1	QREB_MOUSE
31	44	39.4	1217	1	QREB_MOUSE
32	44	39.4	1217	1	QREB_MOUSE
33	44	39.4	1217	1	QREB_MOUSE
34	44	39.4	1217	1	QREB_MOUSE
35	44	39.4	1217	1	QREB_MOUSE
36	44	39.4	1217	1	QREB_MOUSE
37	44	39.4	1217	1	QREB_MOUSE
38	44	39.4	1217	1	QREB_MOUSE
39	44	39.4	1217	1	QREB_MOUSE
40	44	39.4	1217	1	QREB_MOUSE
41	44	39.4	1217	1	QREB_MOUSE
42	44	39.4	1217	1	QREB_MOUSE
43	44	39.4	1217	1	QREB_MOUSE
44	44	39.4	1217	1	QREB_MOUSE
45	44	39.4	1217	1	QREB_MOUSE

QREB_BOVIN	44	43	48.7	593	1	SIB2 CANEA	QREB_BOVIN
QREB_MOUSE	45	43	48.7	593	1	SIB2 CANEA	QREB_MOUSE
QREB_HUMAN	46	43	48.7	593	1	SIB2 CANEA	QREB_HUMAN
QREB_RAT	47	43	48.7	593	1	SIB2 CANEA	QREB_RAT
QREB_MOUSE	48	43	48.7	1141	1	SIB2 CANEA	QREB_MOUSE
QREB_HUMAN	49	43	48.7	1141	1	SIB2 CANEA	QREB_HUMAN
QREB_RAT	50	43	48.7	1141	1	SIB2 CANEA	QREB_RAT
QREB_MOUSE	51	42	47.8	1454	1	SIB2 CANEA	QREB_MOUSE
QREB_HUMAN	52	42	47.8	1454	1	SIB2 CANEA	QREB_HUMAN
QREB_RAT	53	42	47.8	1454	1	SIB2 CANEA	QREB_RAT
QREB_MOUSE	54	42	47.8	1454	1	SIB2 CANEA	QREB_MOUSE
QREB_HUMAN	55	42	47.8	1454	1	SIB2 CANEA	QREB_HUMAN
QREB_RAT	56	42	47.8	1454	1	SIB2 CANEA	QREB_RAT

## ALIGNMENTS

QREB_BOVIN	44	43	48.7	593	1	SIB2 CANEA	QREB_BOVIN
QREB_MOUSE	45	43	48.7	593	1	SIB2 CANEA	QREB_MOUSE
QREB_HUMAN	46	43	48.7	593	1	SIB2 CANEA	QREB_HUMAN
QREB_RAT	47	43	48.7	593	1	SIB2 CANEA	QREB_RAT
QREB_MOUSE	48	43	48.7	1141	1	SIB2 CANEA	QREB_MOUSE
QREB_HUMAN	49	43	48.7	1141	1	SIB2 CANEA	QREB_HUMAN
QREB_RAT	50	43	48.7	1141	1	SIB2 CANEA	QREB_RAT
QREB_MOUSE	51	42	47.8	1454	1	SIB2 CANEA	QREB_MOUSE
QREB_HUMAN	52	42	47.8	1454	1	SIB2 CANEA	QREB_HUMAN
QREB_RAT	53	42	47.8	1454	1	SIB2 CANEA	QREB_RAT
QREB_MOUSE	54	42	47.8	1454	1	SIB2 CANEA	QREB_MOUSE
QREB_HUMAN	55	42	47.8	1454	1	SIB2 CANEA	QREB_HUMAN
QREB_RAT	56	42	47.8	1454	1	SIB2 CANEA	QREB_RAT

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DR EMBL: X57031; CAA0347.1; -;  
DR EMBL: AF06042; AAB6238.1; -;  
DR PIR: S24007; S24007;  
DR InterPro: IPR001630; Leuzip\_CREB;  
DR InterPro: IPR004827; TF\_bZIP.  
DR InterPro: IPR003102; PKID.  
DR Pfam: PF00170; bZIP; 1;  
DR Pfam: PF02173; PKID; 1;  
DR SMART: PR00341; LEUZIP\_CREB;  
DR PROSITE: PS00046; bZIP\_BASIC; 1;  
KW Transcription regulation; DNA-binding; Activator; Phosphorylation;  
KW Nuclear protein;  
FT DNA\_BIND 28 293 BASIC MOTIF;  
FT DOMAIN 296 316 FUNCTION\_ZIPPER;  
FT CONFLICT 63 63 SE 1; 12 (IN REF. 1)  
SQ SEQUENCE 325 AA; 34877 MW; 6364B424FAB474B CRC64.

Query Match 83.8%; Score 93; DB 1; Length 325;  
Best local similarity 100.0%; Freq. No. 4e 07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 4 EILSRPSYRKILNLDSSD 22  
IIIIIIIIIIIIIIIIIIII  
ID 110 EILSRPSYRKILNLDSSD 128

## RESULT 2

CREB\_HUMAN  
ID CREB\_HUMAN STANDARD; PRT; 341 AA.  
AC P16220; P21944; Q9UMA7;  
DT 01-APR-1990 (Ref. 14, Created)  
DT 01-MAY-1991 (Ref. 18, Last sequence update)  
DT 15-JUN-2002 (Ref. 41, Last annotation update)  
DE CAMP response element binding protein (CREB).  
GN CREB1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:90219091; PubMed:2142529;  
RA Berkowitz J A, Gilman M Z;  
RT "Two distinct forms of active transcription factor CREB (cAMP  
RT response element binding protein).";  
PL Proc. Natl. Acad. Sci. U.S.A. 97:5259-5262(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:90416112; PubMed:2196176;  
RA Yoshimura T, Fujisawa J F, Yoshida M J;  
RT "Multiple cDNA clones encoding nuclear proteins that bind to the tax-  
RT dependent enhancer of HTLV-1; all contain a leucine zipper structure  
RT and basic amino acid domain.";  
PL EMBO J. 9:2537-2542(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:92097371; PubMed:1966745.  
RA Wasber G, Meyer T E, Hechtler J F, Habener J F;  
RT "Diversification of cyclic AMP-responsive enhancer binding proteins -  
RT generated by alternative exon splicing.";  
RL Trans. Assoc. Am. Physicians 103:28-37(1999).  
RN [4]  
RP SEQUENCE OF 1 97 AND 102-341 FROM N.A.  
RX MEDLINE:89072714; PubMed:2974179;

RA Hechtler J F, Meyer T E, Van V, Jaenison J L, Habener J F;  
RT "Cyclic AMP-responsive DNA binding protein. Structure based on a  
RT cloned placental cDNA.";  
PL Science 242:1430-1433(1988).  
RN [5]  
RP SEQUENCE OF 1 97 AND 102-341 FROM N.A.  
RX MEDLINE:9134144; PubMed:1831259;  
RA Thimmappa B, Manohar C F, Furlado M R, Ghadue G D, Wolinsky S M;  
RT "Nucleotide and derived amino acid sequences of the CRE-binding  
RT proteins from rat C6 glioma and HeLa cells.";  
PL Nucleic Acids Res. 19:4290-4290(1991).  
RN [6]  
RP SEQUENCE OF 1 9 FROM N.A.  
RX MEDLINE:93145890; PubMed:8381074;  
FA Meyer T E, Wacker C, Van J, Beckmann W, Habener J F;  
RT "The promoter of the gene encoding 3',5'-cyclic adenosine  
RT monophosphate (cAMP) response element binding protein contains  
RT cAMP response elements: evidence for positive autoregulation of gene  
RT transcription.";  
PL Endocrinology 132:770-780(1993).  
CC 1 FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE).  
CC A SEQUENCE ELEMENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREB  
CC STIMULATES TRANSCRIPTION OR BINDING TO THE CRE.  
CC 1 SUBUNIT: BINDS DNA AS A DIMER.  
CC 1-1 SUBCELLULAR LOCATION: Nuclear.  
CC 1-1 ALTERNATIVE PRODUCTS: 2 ISOFORMS: CREB-A (SHOWN HERE) AND CREB-  
CC B. ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC 1 PFM: STIMULATED BY PHOSPHORYLATION.  
CC 1-1 SIMILARITY: BELONGS TO THE bZIP FAMILY.  
CC -----  
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EMBL: S73459; AAR20597.1; -;  
EMBL: X55545; CAA49151.1; -;  
EMBL: S74359; AAA45717.1; -;  
EMBL: M44356; AAA45716.1; -;  
EMBL: M27691; AAA45715.1; -;  
EMBL: X60003; CAA42620.1; -;  
EMBL: S53724; AAD13869.1; -;  
PIR: A35769; A35769;  
PIR: B35769; B35769;  
PIR: B37340; B37340;  
PIR: S12561; S12561;  
PIR: S22398; S22398;  
TRANSFAC: T00163; -;  
TRANSFAC: T00166; -;  
GeneW: HGNC:2345; CREB1.  
MIM: 124810; -;  
InterPro: IPR001630; Leuzip\_CREB;  
InterPro: IPR004827; TF\_bZIP.  
InterPro: IPR003102; PKID.  
Pfam: PF00170; bZIP; 1;  
Pfam: PF02173; PKID; 1;  
PROSITE: PR00341; LEUZIP\_CREB;  
SMART: SM00348; bZIP\_BASIC; 1;  
PROSITE: PS00046; bZIP\_BASIC; 1;  
KW Transcription regulation; DNA-binding; Activator; Phosphorylation;  
KW Nuclear protein; Alternative splicing;  
FT DNA\_BIND 284 305 BASIC MOTIF;  
FT DOMAIN 311 342 LEUCINE\_ZIPPER;  
FT VAAPSLIC 98 101 LEUCINE (IN ISOFORM CREB B).  
FT CONFLICT 4 4 E > D (IN REF. 5).  
FT CONFLICT 8 9 E > D (IN REF. 5).  
FT CONFLICT 160 160 T > A (IN REF. 5).  
FT CONFLICT 167 167 T > A (IN REF. 5).  
FT CONFLICT 159 159 T > A (IN REF. 5).

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F1 C0NF117 176 176 5 176 (IN REF. 5)
F1 C0NF117 184 184 5 184 (IN REF. 5)
F1 C0NF117 188 188 5 188 (IN REF. 5)
F1 C0NF117 195 195 5 195 (IN REF. 5)
F1 C0NF117 210 210 5 210 (IN REF. 5)
SQ SEQUENCE 441 AA: 36606 MW: 15598 IAP40HF6AF CR664;

Query Match: 83.86; Score 9.3; DB 1; Length 441;
Best Local Similarity: 100.0%; Pred. No. 4, 6e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 4 EILSRRSYRKLNLSND 22
DB 126 EILSRRSYRKLNLSND 144

RESULT 4
C0NF117
ID C0NF117 STANDARD: PRI: 441 AA.
AC P15337;
DT 01 APR 1990 (Rel. 14, Created)
DT 01 APR 1990 (Rel. 14, Last sequence update)
DT 15 JUN 2002 (Rel. 41, Last annotation update)
DE CAMP response element binding protein (CREB).
GN CREB1 OR CREB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NWI TaxID 10090;
RN 111
SQ SEQUENCE FROM N.A.
RX MEDLINE 9422489; PubMed 153935;
PA Robert S. Cole, L.J., Beshart M., Schmid E., Schuetz G.,
"Multiple mRNA isoforms of the transcription activator protein CREB:
generation by alternative splicing and specific expression in primary
cell types."
RL Genomics 13(9/4):624(1992).
CS 1 FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE).
CC A SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREB
CC STIMULATES TRANSCRIPTION ON BINDING TO THE CRE.
CC 1 SUBUNIT: BINDS DNA AS A DIMER.
CC 1 SUBCELLULAR LOCATION: Nuclear.
CC 1 ALTERNATIVE SPLICING. AT LEAST SIX FORMS OF CREB ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC 1 PIM: STIMULATED BY PHOSPHORYLATION.
CC 1 SIMILARITY: BELONGS TO THE CRE1 FAMILY.

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EMBL: X67724; CAA47954.1; JOINED.
EMBL: X67725; CAA47954.1; JOINED.
EMBL: X67726; CAA47954.1; JOINED.
EMBL: X67727; CAA47954.1; JOINED.
EMBL: X67728; CAA47954.1; JOINED.
EMBL: M95106; AAA87456.1; JOINED.
F1R: SA2699; SA2699.
TRANSFAC: T01411;
MGD: MGI:88494; Creb1.
InfoPro: I06001630; GenZIp CREB.
InfoPro: I06004827; F4Z1P.
InfoPro: I06003102; PKID.
Pfam: PF00170; bZIP; 1.
Pfam: PF02175; PKID; 1.
PRINTS: PR00041; DEZ1PFRPFR.
SMART: SM00398; bZIP_BASIC; 1.
PROSITE: PS00046; bZIP_BASIC; 1.
KW Transcription regulation; DNA-binding; Activation; Phosphorylation;
KW Nuclear protein; Alternative splicing.
FT DNA-BIND 284 309 BASIC MOTIF (BY SIMILARITY).
FT DOMAIN 311 342 LEU-TIP ZIPPER (BY SIMILARITY).
FT VARSPIC 88 101 MISSING (IN ISOFORM CREB-DELTA).
SQ SEQUENCE 441 AA: 36674 MW: 392968DE9174966A CR664;

Query Match: 83.86; Score 9.3; DB 1; Length 441;
Best Local Similarity: 100.0%; Pred. No. 4, 6e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 4 EILSRRSYRKLNLSND 22
DB 126 EILSRRSYRKLNLSND 144

RESULT 4
CREB1
ID CREB1 STANDARD: PRI: 441 AA.
AC P15337;
DT 01 APR 1990 (Rel. 14, Created)
DT 01 APR 1990 (Rel. 14, Last sequence update)
DT 15 JUN 2002 (Rel. 41, Last annotation update)
DE CAMP-response element binding protein (CREB).
GN CREB1 OR CREB1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NWI TaxID 10116;
RN 111
SQ SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE 8914746; PubMed 2521922;
PA Gonzalez G.A., Yamamoto R.F., Fischer W.H., Barr D., Bengel P.,
Riggs W. 111, Vale W.W., Montminy M.R.
DE "A cluster of phosphorylation sites on the cyclic AMP regulated
nuclear factor CREB predicted by its sequence."
RL Nature 337(739):752(1989).
RN 121
SQ SEQUENCE OF 1-87 AND 102-441 FROM N.A. (DELTA 130-608).
RX MEDLINE 9134144; PubMed 1831296;
PA Short M.L., Manchay C.F., Furlan R.R., Gladys G.D., Wiatersky S.M.,
Thimmapaya B., Juchman K.A.;
DE "Sequence of rat protein amino acid sequences of the CRE binding
protein from rat 36 plasmid and Bcl-1 cells."
RL Nucleic Acids Res. 19(4290):4290(1991).
CC 1 FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE).
CC A SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREB
CC STIMULATES TRANSCRIPTION ON BINDING TO THE CRE.
CC 1 SUBUNIT: BINDS DNA AS A DIMER.
CC 1 SUBCELLULAR LOCATION: Nuclear.
CC 1 ALTERNATIVE SPLICING. TWO FORMS OF CREB CAN BE GENERATED BY
CC ALTERNATIVE SPLICING.
CC 1 PIM: STIMULATED BY PHOSPHORYLATION.
CC 1 SIMILARITY: BELONGS TO THE CRE1 FAMILY.

```









KW Protein structure, 3D relationship, DNA related, Nuclear protein, Basic, MAF, (BY SIMILARITY).  
 FI DNA BIND 219 249  
 LEADLINE ZIPPER (BY SIMILARITY).  
 SQ SEQUENCE 249 AA; 2756 MW; 98996A5B2F79A0B C6C64;

Query Match 67.6%; Score 75; DB 1; Length 249;  
 Best Local Similarity 83.6%; Pred. No. 0.00019;  
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

27 4 EILSPSPSPKILNLSLSD 22  
 LIIIIIIIIIIIIIIIIII  
 60 EILAPPSYPRIGLILALG 74

RESULT 11  
 ATFL\_MOUSE  
 ID ATFL\_MOUSE STANDARD; PRI: 249 AA;  
 AC P61299;  
 DI 15 JUL 1998 (rel. 36, created)  
 DI 15 JUL 1998 (rel. 36, last sequence update)  
 DI 16 OCT 2001 (rel. 43, last annotation update)  
 DE Cyclic AMP dependent transcription factor ATF 1 (Activating  
 DE transcription factor 1) (TF ATF1).  
 GN ATF1  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
 OX NCBI\_TaxID 10091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 9216656; PubMed 151847;  
 RA Lee M. R., Choudhry S., Lion M. L., Wu M., Li W., F., Beach Y., P.,  
 RA Bai M. Z.;  
 RI "Isolation and characterization of nuclear proteins that bind to T  
 RI cell receptor V beta decamer motif."  
 RI J. Immunol. 145:1906-1912(1992).  
 CC 1 FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)  
 CC (CONSENSUS: 5'-GACAGTCA-3') A 1.6 kbT of 19. IN MANY  
 CC VIRAL AND CELLULAR PROMOTERS. BINDS TO THE TAX-RESPONSIVE ELEMENT  
 CC (TRE) OF HIV-1.  
 CC 1 SUBUNIT: BINDS DNA AS A DIMER (BY SIMILARITY).  
 CC 1 SUBCELLULAR LOCATION: Nuclear.  
 CC 1 SIMILARITY: BELONGS TO THE bZIP FAMILY. ATF SUBFAMILY.

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EMBL: M63725; AAA00055.1;  
 M63725; M63725; A111;  
 InterPro: IPR001640; Leuzip\_CHEB;  
 InterPro: IPR004927; TF bZIP;  
 InterPro: IPR033623; PKID;  
 Pfam: PF00170; bZIP; 1;  
 Pfam: PF02173; PKID; 1;  
 PRINTS: PR00041; LEUZIP\_CHEB;  
 SMART: SM00336; bZIP; 1;  
 PROSITE: PS00046; bZIP\_BASIC; 1;  
 TRANSIT: PS00041; LEUZIP\_CHEB;  
 LEUZIP\_BASIC; 1;  
 DNA BIND 219 249  
 LEADLINE ZIPPER;  
 DOMAIN 249 249  
 SEQUENCE 249 AA; 2924 MW; 066526515964A0 C6C64;

Query Match 67.6%; Score 75; DB 1; Length 249;  
 Best Local Similarity 83.6%; Pred. No. 0.00021;  
 Matches 15; Conservative 27; Mismatches 1; Indels 0; Gaps 0;

27 5 ILAPPSYPRIGLILALG 22  
 LIIIIIIIIIIIIIIIIII

16 57 ILAPPSYPRIGLILALG 74

RESULT 12  
 ATFL\_HUMAN

ID ATFL\_HUMAN STANDARD; PRI: 271 AA;  
 AC P18846; P25168;  
 DI 01 NOV 1990 (rel. 16, created)  
 DI 01 NOV 1990 (rel. 22, last sequence update)  
 DI 16 OCT 2001 (rel. 40, last annotation update)  
 DE Cyclic AMP-dependent transcription factor ATF 1 (Activating  
 DE transcription factor 1) (TFB46 protein).  
 GN ATF1  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;  
 OX NCBI\_TaxID 9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 9041612; PubMed 2196176;  
 RA Yoshimura T., Fujisawa J. I., Yoshida M.;  
 RI "Multiple cDNA clones encoding nuclear proteins that bind to the tax  
 RI dependent enhancer of HIV 1: all contain a longline zipper structure  
 RI and basic amino acid domain."  
 RI EMBO J. 9:2547-2552(1990).  
 RN [2]  
 RP SEQUENCE OF 49-271 FROM N.A.  
 RX MEDLINE 90185187; PubMed 2516827;  
 RA Bai M., Li W., Conkos W., Green M. R.;  
 RI "Transcription factor ATF cDNA clones: an extensive family of longline  
 RI zipper proteins able to selectively form DNA binding heterodimers."  
 RI Genes Dev. 3:2083-2090(1989).  
 RN [3]  
 RP FRATUM.  
 RA Bai M., Li W., Conkos W., Green M. R.;  
 RI Genes Dev. 4:682-682(1990).  
 CC 1 FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)  
 CC (CONSENSUS: 5'-GACAGTCA-3') A 1.6 kbT of 19. IN MANY  
 CC VIRAL AND CELLULAR PROMOTERS. BINDS TO THE TAX-RESPONSIVE ELEMENT  
 CC (TRE) OF HIV-1.  
 CC 1 SUBUNIT: BINDS DNA AS A DIMER.  
 CC 1 SUBCELLULAR LOCATION: Nuclear.  
 CC 1 SIMILARITY: BELONGS TO THE bZIP FAMILY. ATF SUBFAMILY.

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 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).

EMBL: X55544; CAA39150.1;  
 F18; S12560; S12560;  
 F18; A4223; A4223;  
 TRANSFAC; T09768; 1;  
 Genew; H083783; ATF1;  
 MIM; 124803; 1;  
 InterPro: IPR001640; Leuzip\_CHEB;  
 InterPro: IPR004927; TF bZIP;  
 InterPro: IPR033623; PKID;  
 Pfam: PF00170; bZIP; 1;  
 Pfam: PF02173; PKID; 1;  
 PRINTS: PR00041; LEUZIP\_CHEB;  
 SMART: SM00336; bZIP; 1;  
 PROSITE: PS00046; bZIP\_BASIC; 1;  
 TRANSIT: PS00041; LEUZIP\_CHEB;  
 LEUZIP\_BASIC; 1;  
 DNA BIND 219 249  
 LEADLINE ZIPPER;  
 DOMAIN 241 262  
 HOMO A (IN REF. 2).  
 CONFILIC 227 227  
 MISSING (IN REF. 2).  
 SEQUENCE 271 AA; 2924 MW; 0470102441E13 C6C64;





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Genome version 5.1.3  
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CM protein protein search, using sw model

Run on: January 2, 2003, 12:26:41 : Search time: 32 seconds  
(without alignments)  
69.097 Million cell updates/sec

Hit loc: US 09 786 417-1

Perfect score: 111

Sequence: 1 TSSGRLSPRRSYRKLLNLSST 23

Scoring table: BL-SUM62

Gap 10, 0 : Gapext 0.5

Searched: 284224 ceps, 9614422 residues

Total number of hits satisfying chosen parameters: 284224

Minimum hit used length: 6

Maximum hit seq length: 200000000

Post processing: Minimum Match 90

Maximum Match 100

Listing first 45 summaries

Database:

PIR 733\*

13 pir13\*

23 pir23\*

33 pir33\*

43 pir43\*

Prod. No. is the number of results predicted by changes to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the full score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	Id	Description
1	93	83.8	417	2	hypothetical prote
2	93	83.8	425	2	CAMP response elem
3	93	83.8	426	2	CAMP-responsive on
4	93	83.8	427	2	CAMP response elem
5	93	83.8	427	2	regulatory protein
6	93	83.8	427	2	CAMP response elem
7	93	83.8	441	2	hypothetical prote
8	93	83.8	441	2	CAMP response elem
9	93	83.8	441	2	CAMP response elem
10	99	81.1	423	2	CAMP response elem
11	89	80.2	217	2	CAMP response elem
12	89	80.2	220	2	CAMP response elem
13	89	80.2	229	2	CAMP response elem
14	89	80.2	229	2	CAMP response elem
15	89	80.2	276	2	CAMP response elem
16	89	80.2	441	2	CAMP response elem
17	89	80.2	441	2	CAMP response elem
18	89	80.2	444	2	CAMP response elem
19	89	80.2	444	2	CAMP response elem
20	88	79.3	426	2	CAMP response elem
21	75	67.6	229	2	17kD beta-CRF med
22	75	67.6	271	2	transcription fact
23	58	52.3	331	2	hypothetical prote
24	58	52.3	333	2	hypothetical prote
25	47	42.3	467	2	GMP synthase, pp-A
26	47	42.3	666	1	M50-2 homolog, Bol
27	37	32.3	1999	2	protein, tyrosine k
28	37	42.3	1100	2	protein-tyrosine k
29	47	42.3	1299	2	158401

# ALIGNMENTS

## RESULT 1

S42702

hypothetical protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 08 Dec-2000

C:Accession: S42702

Requert, S.; Cole, T.J.; Boshart, M.; Schmid, E.; Schuetz, G.

EMBL J. 11, 1503-1512, 1992

A:Title: Multiple mRNA isoforms of the transcription and factor protein CREB: genomic

A:Reference number: S20955; MIM:92244889; PMID:154295

A:Accession: S42702

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-417-ROP

A:Cross references: PMID:87726

C:Genetic:

A:Feature: 493-533, 533-593, 593-771

C:Superfamily: fos/jun DNA-binding domain homology

Query Match 83.8% Score 93: 416-23 Length 417:

Best local similarity 100.0% Prod. No. 7.4e 07:

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ELSSRSYRKLLNLSST 22

112 ELSSRSYRKLLNLSST 140

## RESULT 2

S24007

CAMP response element-binding protein CREB-2 bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 08 Jun 1994 #sequence\_revision 16 Nov 1995 #text\_change 05 Nov 1999

C:Accession: S24007

Kimmins, L.; Kottmann, R.; Chen, G.; Perletti, D.; Bortny, A.; Morse, D.

UNA Seq. 1, 415-417, 1991

A:Title: Recombinant sequence of the bovine c-fos-like DNA-binding protein

A:Reference number: S24007; MIM:92119333; PMID:1607490

A:Accession: S24007

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-425-WLL

A:Cross references: EMBL:877131, NID:8205, FID:85545047.1; FID:8206

C:Superfamily: fos/jun DNA-binding domain homology

C:Keywords: DNA binding; transcription domain regulation

F.25.3 fos/jun-like, fos/jun DNA-binding domain homology - FID:

Query Match 83.8% Score 93: 146-23 Length 425:

Best local similarity 100.0% Prod. No. 7.4e 07:

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ELSSRSYRKLLNLSST 22

Db 110 EILSRPSPYKILINDLSSD 129  
|||||

## RESULT 3

A40120

CAMP-responsive enhancer-binding protein CREB human

C:Species: Homo sapiens (man)

C:Date: 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 10-Oct-1997

C:Accession: A40120

R:Boettlinger, J.P.; Meyer, T.E.; Yan, Y.; Jameson, J.L.; Habener, J.F.

Science 242, 1430-1433, 1988

A:Title: Cyclic AMP-responsive DNA binding protein structure based on a cloned cDNA

A:Keywords: CREB; DNA binding; transcription; cAMP

A:Accession: A40120

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-326 &lt;RUP&gt;

A:Cross references: GR M27691

C:Superfamily: fos/jun DNA-binding domain homology

F:240-403/Genbank: fos/jun DNA-binding domain homology &lt;RUP&gt;

Query Match 83.8% Score 93; DP 2; Length 326;

Best Local Similarity 100.0%; Pred. No. 7.6e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPYKILINDLSSD 22

|||||

Db 111 EILSRPSPYKILINDLSSD 129

## RESULT 4

A3769

CAMP response element binding protein A - human

C:Species: Homo sapiens (man)

C:Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 21-Jul-2003

C:Accession: A37440; A3769

R:Maeder, G.; Meyer, T.E.; Hoeflinger, J.P.; Habener, J.F.

Trans. Assoc. Am. Physicians 103, 29-37, 1990

A:Title: Purification of cyclic AMP response element binding proteins generated by

A:Reference number: A37340, MIMD.92087471, PMID.1966745

A:Accession: A37440

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-327 &lt;WAE&gt;

A:Cross references: GR S2459, RIF.1243429; FIDR.AAP20597.1, FIDR.3219129

P:Kozlitz, L.A.; Gilman, M.C.

Proc. Natl. Acad. Sci. U.S.A. 87, 5258-5262, 1990

A:Title: Two distinct forms of active transcription factor CREB (CAMP response element b

A:Reference number: A3769, MIMD.9319591; PMID.2142528

A:Accession: A3769

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-327 &lt;RER&gt;

A:Cross references: GR M43456; NID-q181042; PIDR.AAA35716.1; PID-q181043

C:Superfamily: fos/jun DNA-binding domain homology

C:Keywords: alternative splicing; DNA binding; transcription regulation

F:241-404/Genbank: fos/jun DNA-binding domain homology &lt;RUP&gt;

Query Match 83.8% Score 93; DP 2; Length 327;

Best Local Similarity 100.0%; Pred. No. 7.6e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPYKILINDLSSD 22

|||||

Db 112 EILSRPSPYKILINDLSSD 130

## RESULT 5

S20955

regulatory protein CREB - mouse

N:Alternate names: cAMP responsive element binding protein

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 10-Oct-1997

C:Accession: S20955

R:Ruppert, S.; Cole, T.J.; Roshart, M.; Schmid, E.; Schuetz, G.

EMBO J. 11, 1503-1512, 1992

A:Title: Multiple mRNA isoforms of the transcription activator protein CREB: generati

A:Reference number: S20955; MIMD.92224889; PMID.1529295

A:Accession: S20955

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 &lt;RUP&gt;

A:Cross references: EMBL:X67727

C:Genetics:

A:Title: Multiple mRNA isoforms of the transcription activator protein CREB: generati

A:Reference number: S20955; MIMD.92224889; PMID.1529295

A:Accession: S20955

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 &lt;RUP&gt;

A:Cross references: EMBL:X67727

C:Genetics:

A:Title: Multiple mRNA isoforms of the transcription activator protein CREB: generati

A:Reference number: S20955; MIMD.92224889; PMID.1529295

A:Accession: S20955

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 &lt;RUP&gt;

A:Cross references: EMBL:X67727

C:Genetics:

A:Title: Multiple mRNA isoforms of the transcription activator protein CREB: generati

A:Reference number: S20955; MIMD.92224889; PMID.1529295

A:Accession: S20955

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 &lt;RUP&gt;

A:Cross references: EMBL:X67727

C:Genetics:

A:Title: Multiple mRNA isoforms of the transcription activator protein CREB: generati

A:Reference number: S20955; MIMD.92224889; PMID.1529295

A:Accession: S20955

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 &lt;RUP&gt;

A:Cross references: EMBL:X67727

C:Genetics:

A:Title: Multiple mRNA isoforms of the transcription activator protein CREB: generati

A:Reference number: S20955; MIMD.92224889; PMID.1529295

A:Accession: S20955

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 &lt;RUP&gt;

A:Cross references: EMBL:X67727

C:Genetics:

A:Title: Multiple mRNA isoforms of the transcription activator protein CREB: generati

A:Reference number: S20955; MIMD.92224889; PMID.1529295

A:Accession: S20955

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 &lt;RUP&gt;

A:Cross references: EMBL:X67727

C:Genetics:

A:Title: Multiple mRNA isoforms of the transcription activator protein CREB: generati

A:Reference number: S20955; MIMD.92224889; PMID.1529295

A:Accession: S20955

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 &lt;RUP&gt;

A:Cross references: EMBL:X67727

C:Genetics:

A:Title: Multiple mRNA isoforms of the transcription activator protein CREB: generati

A:Reference number: S20955; MIMD.92224889; PMID.1529295

A:Accession: S20955

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 &lt;RUP&gt;

A:Cross references: EMBL:X67727

C:Genetics:





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AltTitle: CREM gene: use of alternative DNA-binding domains generates multiple antagonists
A:Reference number: A37944; MIM:91145994; PMID:1847666
A:Accession: U37944
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <PDB>
A:Cross-references: GB:M60285; NID:q192716; PID:AA17496.1; PID:q192717
C:Superfamily: fos/jun DNA-binding domain homology
F:151-194/Domain: fos/jun DNA-binding domain homology <PDB>

Query Match 80.2% Score 89; DB 2; Length 229;
Best Local Similarity 94.7% Pred. No. 2.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPVSYPKILNELSSD 22
      |||
DB 61 EILSRPVSYPKILNELSSD 79

RESULT 12
S26685
CAMP response element modulator CREM - human (fragment)
C:Species: Homo sapiens (man)
C:Dates: 07-Oct-1994 #sequence_revision 37-Oct-1994 #text_change 21 Jul-2000
C:Accession: S26685
R:Meyer, T.E.; Habener, J.F.
Nucleic Acids Res. 20, 6105, 1992
A:Title: Cyclic AMP response element binding protein CREB and modulator protein CREM are
A:Reference number: S26685; MIM:93096608; PMID:1461747
A:Accession: S26685
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-220 <MEY>
A:Cross-references: EMBL:Z15159; NID:q30276; PID:CAA78958.1; PID:q40217
A:Note: this sequence was submitted to the PubMed data library, September 1992
C:Genetics:
A:Gene: GDB:CREM
A:Cross-references: GDB:269801
A:Map position: 10p12.1-10p11.2
C:Superfamily: fos/jun DNA-binding domain homology
C:Keywords: DNA binding; heterodimer; leucine zipper; transcription factor
F:154-197/Domain: fos/jun DNA-binding domain homology <PDB>

Query Match 80.2% Score 89; DB 2; Length 229;
Best Local Similarity 94.7% Pred. No. 2.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPVSYPKILNELSSD 22
      |||
DB 64 EILSRPVSYPKILNELSSD 82

RESULT 13
B47944
CAMP response element-binding protein beta mouse
C:Species: Mus musculus (house mouse)
C:Dates: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 05-Nov-1999
C:Accession: B47944
R:Foulkes, N.S.; Borrelli, E.; Sassone-Corsi, P.
Cell 64, 739-749, 1991
A:Title: CREM gene: use of alternative DNA binding domains generates multiple antagonists
A:Reference number: A37944; MIM:91145994; PMID:1847666
A:Accession: B47944
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-229 <FOU>
A:Cross-references: GB:M60285; NID:q192716; PID:AA17496.1; PID:q192718
C:Superfamily: fos/jun DNA-binding domain homology
F:163-206/Domain: fos/jun DNA-binding domain homology <PDB>

Query Match 80.2% Score 89; DB 2; Length 229;
Best Local Similarity 94.7% Pred. No. 2.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 4 EILSRPVSYPKILNELSSD 22
      |||
DB 61 EILSRPVSYPKILNELSSD 79

RESULT 14
A37944
CAMP response element-binding protein alpha mouse
C:Species: Mus musculus (house mouse)
C:Dates: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 05-Nov-1999
C:Accession: A37944
R:Foulkes, N.S.; Borrelli, E.; Sassone-Corsi, P.
Cell 64, 739-749, 1991
A:Title: CREM gene: use of alternative DNA binding domains generates multiple antagonists
A:Reference number: A37944; MIM:91145994; PMID:1847666
A:Accession: A37944
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-229 <FOU>
A:Cross-references: GB:M60285; NID:q192716; PID:AA17497.1; PID:q192719
C:Superfamily: fos/jun DNA-binding domain homology
C:Keywords: alternative splicing; DNA binding; transcription regulation
F:163-206/Domain: fos/jun DNA-binding domain homology <PDB>

Query Match 80.2% Score 89; DB 2; Length 229;
Best Local Similarity 94.7% Pred. No. 2.2e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPVSYPKILNELSSD 22
      |||
DB 61 EILSRPVSYPKILNELSSD 79

RESULT 15
S36101
CAMP response element-binding protein epsilon mouse
N:Alternate names: cAMP-responsive element modulator epsilon
C:Species: Mus musculus (house mouse)
C:Dates: 20-Dec-1993 #sequence_revision 10-Jun-1995 #text_change 05-Nov-1999
C:Accession: S36101
R:Rothblatt, J.; Liska, S.; Montminy, M.
Nature 364, 821-824, 1993
A:Title: Protein kinase A dependent activation of transcription factor CREB reveals its
A:Reference number: S36101; MIM:93361150; PMID:8102791
A:Accession: S36101
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-278 <BRP>
A:Cross-references: GB:S64790; NID:q102276; PID:AAB27893.1; PID:q102297
C:Superfamily: fos/jun DNA-binding domain homology
F:212-255/Domain: fos/jun DNA-binding domain homology <PDB>

Query Match 80.2% Score 89; DB 2; Length 278;
Best Local Similarity 94.7% Pred. No. 2.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPVSYPKILNELSSD 22
      |||
DB 110 EILSRPVSYPKILNELSSD 128

Search completed: January 2, 2003, 12:29:15
Job time : 33 secs

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us-09-786-317-1.rapn

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us-09-786-317-1.rapn

# SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	us-09-786-317-1	84.8	58	6	US-10-211-088-105		Sequence 105, App
2	us-09-786-317-1	84.8	115	6	US-10-211-088-426		Sequence 426, App
3	us-09-786-317-1	89.2	137	5	US-09-724-676-67411		Sequence 67411, A
4	us-09-786-317-1	89.2	137	5	US-09-724-676-67411		Sequence 67411, A
5	us-09-786-317-1	89.2	175	5	US-09-724-676-67425		Sequence 67425, A
6	us-09-786-317-1	89.2	175	5	US-09-724-676-67425		Sequence 67425, A
7	us-09-786-317-1	89.2	175	5	US-09-724-676-67425		Sequence 67425, A
8	us-09-786-317-1	89.2	175	5	US-09-724-676-67425		Sequence 67425, A
9	us-09-786-317-1	89.2	186	5	US-09-724-676-67426		Sequence 67426, A
10	us-09-786-317-1	89.2	186	5	US-09-724-676-67426		Sequence 67426, A
11	us-09-786-317-1	89.2	190	5	US-09-724-676-67419		Sequence 67419, A
12	us-09-786-317-1	89.2	190	5	US-09-724-676-67427		Sequence 67427, A
13	us-09-786-317-1	89.2	224	5	US-09-724-676-67427		Sequence 67427, A
14	us-09-786-317-1	89.2	224	5	US-09-724-676-67427		Sequence 67427, A
15	us-09-786-317-1	89.2	224	5	US-09-724-676-67427		Sequence 67427, A
16	us-09-786-317-1	89.2	224	5	US-09-724-676-67427		Sequence 67427, A
17	us-09-786-317-1	89.2	239	5	US-09-724-676-67404		Sequence 67404, A
18	us-09-786-317-1	89.2	239	5	US-09-724-676-67404		Sequence 67404, A
19	us-09-786-317-1	89.2	241	5	US-09-724-676-67405		Sequence 67405, A
20	us-09-786-317-1	89.2	241	5	US-09-724-676-67405		Sequence 67405, A
21	us-09-786-317-1	89.2	249	5	US-09-724-676-67414		Sequence 67414, A
22	us-09-786-317-1	89.2	249	5	US-09-724-676-67414		Sequence 67414, A
23	us-09-786-317-1	89.2	249	5	US-09-724-676-67414		Sequence 67414, A
24	us-09-786-317-1	89.2	249	5	US-09-724-676-67414		Sequence 67414, A
25	us-09-786-317-1	89.2	241	5	US-09-724-676-67414		Sequence 67414, A
26	us-09-786-317-1	89.2	241	5	US-09-724-676-67414		Sequence 67414, A

## ALIGNMENTS

### RESULT 1

US-10-211-088-105  
 : Sequence 105, Application US/10211088  
 : GENERAL INFORMATION:  
 : APPLICANT: Bright, Gary R.  
 : APPLICANT: Frankum, D. David  
 : APPLICANT: Chen, Yih Tai  
 : TITLE: INVENTION: Novel Fusion Proteins And Assays For Molecular Binding  
 : FILE NUMBER: 01-1022 US  
 : CURRENT APPLICATION NUMBER: 02/10211088  
 : PRIOR FILING DATE: 2001-08-03  
 : PRIOR APPLICATION NUMBER: 602/41,569  
 : NUMBER OF SEQ ID NOS: 46  
 : SOFTWARE: Patent in version 6.1  
 : SEQ ID NO 105  
 : LENGTH: 58  
 : TYPE: PRT  
 : ORGANISM: Artificial sequence  
 : FEATURE:  
 : OTHER INFORMATION: Binding domain  
 US-10-211-088-105  
 Query Match 84.8%, Score 93, DB 6, Length 58;  
 Best local Similarity 130.0%, Pred. No. 1, Loc 07;  
 Matches 19, Conservat 100, Mismatches 0, Gaps 0;  
 57 4 EILSRREYKRLNLSLS 22  
 DB 22 EILSRREYKRLNLSLS 40  
 R52923 2  
 US-10-211-088-426  
 : Sequence 426, Application US/10211088  
 : GENERAL INFORMATION:  
 : APPLICANT: Bright, Gary R.  
 : APPLICANT: Frankum, D. David  
 : APPLICANT: Chen, Yih Tai  
 : TITLE: INVENTION: Novel Fusion Proteins And Assays For Molecular Binding  
 : FILE NUMBER: 01-1022 US  
 : CURRENT APPLICATION NUMBER: 02/10211088  
 : PRIOR FILING DATE: 2001-08-03  
 : PRIOR APPLICATION NUMBER: 602/41,569  
 : NUMBER OF SEQ ID NOS: 46  
 : SOFTWARE: Patent in version 6.1  
 : SEQ ID NO 426  
 : LENGTH: 58  
 : TYPE: PRT  
 : ORGANISM: Artificial sequence  
 : FEATURE:  
 : OTHER INFORMATION: Binding domain  
 US-10-211-088-426  
 Query Match 84.8%, Score 93, DB 6, Length 58;  
 Best local Similarity 130.0%, Pred. No. 1, Loc 07;  
 Matches 19, Conservat 100, Mismatches 0, Gaps 0;  
 57 4 EILSRREYKRLNLSLS 22  
 DB 22 EILSRREYKRLNLSLS 40  
 R52923 2

1 NUMBER OF SEQ ID NOS: 366  
2 SOFTWARE: PatentIn version 3.1  
3 SEQ ID NO 426  
4 LENGTH: 115  
5 TYPE: PRT  
6 ORGANISM: Artificial Sequence  
7 FEATURE:  
8 OTHER INFORMATION: cAMP dependent protein kinase interaction fusion protein  
US-10-211-099-426

Query Match 80.2% Score 93; DB 6; Length 115;  
Best Local Similarity 90.0%; Pred. No. 3.7e-07;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNLSDD 22

|||||

DB 79 EILSRPSPSYRKILNLSDD 97

1 Sequence 67411 Application US/09/724676  
2 GENERAL INFORMATION:  
3 APPLICANT: Compugen LTD  
4 TITLE OF INVENTION: Variants of alternative splicing  
5 FILE REFERENCE: 129181.4 Compugen  
6 CURRENT APPLICATION NUMBER: US/09/724676  
7 CURRENT FILING DATE: 2000-11-28  
8 NUMBER OF SEQ ID NOS: 97222  
9 SOFTWARE: PatentIn version 3.2  
10 SEQ ID NO 67411  
11 LENGTH: 137  
12 TYPE: PRT  
13 ORGANISM: Homo sapiens  
US-09-724-676-67411

Query Match 80.2% Score 89; DB 5; Length 137;  
Best Local Similarity 94.7%; Pred. No. 1.9e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNLSDD 22

|||||

DB 62 EILSRPSPSYRKILNLSDD 80

1 Sequence 67411 Application US/09/724676A  
2 GENERAL INFORMATION:  
3 APPLICANT: Compugen LTD  
4 TITLE OF INVENTION: Variants of alternative splicing  
5 FILE REFERENCE: 129181.4 Compugen  
6 CURRENT APPLICATION NUMBER: US/09/724676A  
7 CURRENT FILING DATE: 2000-11-28  
8 NUMBER OF SEQ ID NOS: 97222  
9 SOFTWARE: PatentIn version 3.2  
10 SEQ ID NO 67411  
11 LENGTH: 137  
12 TYPE: PRT  
13 ORGANISM: Homo sapiens  
US-09-724-676A-67411

Query Match 80.2% Score 89; DB 5; Length 137;  
Best Local Similarity 94.7%; Pred. No. 1.9e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNLSDD 22

|||||

DB 62 EILSRPSPSYRKILNLSDD 80

RESULT 5  
US-09-724-676-67425

1 Sequence 67425 Application US/09/724676

2 GENERAL INFORMATION:  
3 APPLICANT: Compugen LTD  
4 TITLE OF INVENTION: Variants of alternative splicing  
5 FILE REFERENCE: 129181.4 Compugen  
6 CURRENT APPLICATION NUMBER: US/09/724676  
7 CURRENT FILING DATE: 2000-11-28  
8 NUMBER OF SEQ ID NOS: 97222  
9 SOFTWARE: PatentIn version 3.2  
10 SEQ ID NO 67425  
11 LENGTH: 175  
12 TYPE: PRT  
13 ORGANISM: Homo sapiens  
US-09-724-676-67425

Query Match 80.2% Score 89; DB 5; Length 175;  
Best Local Similarity 94.7%; Pred. No. 2.4e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNLSDD 22

|||||

DB 115 EILSRPSPSYRKILNLSDD 133

1 Sequence 67425 Application US/09/724676  
2 GENERAL INFORMATION:  
3 APPLICANT: Compugen LTD  
4 TITLE OF INVENTION: Variants of alternative splicing  
5 FILE REFERENCE: 129181.4 Compugen  
6 CURRENT APPLICATION NUMBER: US/09/724676  
7 CURRENT FILING DATE: 2000-11-28  
8 NUMBER OF SEQ ID NOS: 97222  
9 SOFTWARE: PatentIn version 3.2  
10 SEQ ID NO 67425  
11 LENGTH: 175  
12 TYPE: PRT  
13 ORGANISM: Homo sapiens  
US-09-724-676-67426

Query Match 80.2% Score 89; DB 5; Length 175;  
Best Local Similarity 94.7%; Pred. No. 2.4e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNLSDD 22

|||||

DB 115 EILSRPSPSYRKILNLSDD 133

1 Sequence 67425 Application US/09/724676A  
2 GENERAL INFORMATION:  
3 APPLICANT: Compugen LTD  
4 TITLE OF INVENTION: Variants of alternative splicing  
5 FILE REFERENCE: 129181.4 Compugen  
6 CURRENT APPLICATION NUMBER: US/09/724676A  
7 CURRENT FILING DATE: 2000-11-28  
8 NUMBER OF SEQ ID NOS: 97222  
9 SOFTWARE: PatentIn version 3.2  
10 SEQ ID NO 67425  
11 LENGTH: 175  
12 TYPE: PRT  
13 ORGANISM: Homo sapiens  
US-09-724-676A-67425

Query Match 80.2% Score 89; DB 5; Length 175;  
Best Local Similarity 94.7%; Pred. No. 2.4e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKILNLSDD 22

|||||

146 11% EILSRPSPYRKLNELSSD 144

RESULT 8

US-09-724-676A-67426

Sequence 67426, Application US/09724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Computer

CURRENT APPLICATION NUMBER: US/09724-676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patent in version 4.2

SEQ ID NO 67426

LENGTH: 176

TYPE: PRT

ORGANISM: Homo sapiens

US-09-724-676A-67426

Query Match

Best Local Similarity 80.2%; Score 89; ID 5; Length 175;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPYRKLNELSSD 22

11% EILSRPSPYRKLNELSSD 144

RESULT 9

US-09-724-676A-67419

Sequence 67419, Application US/09724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Computer

CURRENT APPLICATION NUMBER: US/09724-676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patent in version 4.2

SEQ ID NO 67419

LENGTH: 186

TYPE: PRT

ORGANISM: Homo sapiens

US-09-724-676A-67419

Query Match

Best Local Similarity 80.2%; Score 89; ID 5; Length 186;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPYRKLNELSSD 22

11% EILSRPSPYRKLNELSSD 144

RESULT 10

US-09-724-676A-67419

Sequence 67419, Application US/09724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Computer

CURRENT APPLICATION NUMBER: US/09724-676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patent in version 4.2

SEQ ID NO 67419

LENGTH: 186

TYPE: PRT

ORGANISM: Homo sapiens

US-09-724-676A-67419

Best Local Similarity 94.7%; Score 89; ID 5; Length 190;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPYRKLNELSSD 22

11% EILSRPSPYRKLNELSSD 144

RESULT 11

US-09-724-676A-67427

Sequence 67427, Application US/09724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Computer

CURRENT APPLICATION NUMBER: US/09724-676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patent in version 4.2

SEQ ID NO 67427

LENGTH: 190

TYPE: PRT

ORGANISM: Homo sapiens

US-09-724-676A-67427

Query Match

Best Local Similarity 94.7%; Score 89; ID 5; Length 190;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPYRKLNELSSD 22

11% EILSRPSPYRKLNELSSD 144

RESULT 12

US-09-724-676A-67427

Sequence 67427, Application US/09724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Computer

CURRENT APPLICATION NUMBER: US/09724-676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patent in version 4.2

SEQ ID NO 67427

LENGTH: 190

TYPE: PRT

ORGANISM: Homo sapiens

US-09-724-676A-67427

Query Match

Best Local Similarity 80.2%; Score 89; ID 5; Length 190;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPYRKLNELSSD 22

11% EILSRPSPYRKLNELSSD 144

RESULT 13

US-09-724-676A-67442

Sequence 67442, Application US/09724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Computer

CURRENT APPLICATION NUMBER: US/09724-676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patent in version 4.2

SEQ ID NO 67442

LENGTH: 224

! TYPE: PRI  
! ORGANISM: Homo sapiens  
US-09-724-676-67432

Query Match 80.2%; Score 89; DB 5; Length 224;  
Best Local Similarity 94.7%; Pred. No. 3,2e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKLINLSSD 22  
IIIIIIIIIIIIIIIIIIII  
DB 164 EILSRPSPSYRKLINLSSD 182

## RESULT 14

US-09-724-676-67433

! Sequence 67433, Application US/09724676

! GENERAL INFORMATION:

! APPLICANT: CompuGen Ltd

! TITLE OF INVENTION: Variants of alternative splicing

! FILE REFERENCE: 129181.4 CompuGen

! CURRENT APPLICATION NUMBER: US/09724.676

! CURRENT FILING DATE: 2000 11 28

! NUMBER OF SEQ ID NOS: 97222

! SOFTWARE: Patent In version 3.2

! SEQ ID NO 67433

! LENGTH: 224

! TYPE: PRI

! ORGANISM: Homo sapiens

US-09-724-676-67433

Query Match 80.2%; Score 89; DB 5; Length 224;  
Best Local Similarity 94.7%; Pred. No. 3,2e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKLINLSSD 22  
IIIIIIIIIIIIIIIIIIII  
DB 164 EILSRPSPSYRKLINLSSD 182

## RESULT 15

US-09-724-676A-67432

! Sequence 67432, Application US/09724676A

! GENERAL INFORMATION:

! APPLICANT: CompuGen Ltd

! TITLE OF INVENTION: Variants of alternative splicing

! FILE REFERENCE: 129181.4 CompuGen

! CURRENT APPLICATION NUMBER: US/09724.676A

! CURRENT FILING DATE: 2000 11 28

! NUMBER OF SEQ ID NOS: 97222

! SOFTWARE: Patent In version 3.2

! SEQ ID NO 67432

! LENGTH: 224

! TYPE: PRI

! ORGANISM: Homo sapiens

US-09-724-676A-67432

Query Match 80.2%; Score 89; DB 5; Length 224;  
Best Local Similarity 94.7%; Pred. No. 3,2e-06;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSPSYRKLINLSSD 22  
IIIIIIIIIIIIIIIIIIII  
DB 164 EILSRPSPSYRKLINLSSD 182

Search completed: January 2, 2003, 12:35:49  
Job time : 11.5 secs







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Query Match          R4.0K; Score 94; DB 1; Length 428;
Best Local Similarity 100.0K; Prod. No. 4.6e-06;
Matches 19; Conservatio 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSYRKILNLSND 22
DB 112 EILSRPSYRKILNLSND 140

RESULT 1
US 09 420 060 R
Sequence 2; Application US/09420060
GENERAL INFORMATION:
APPLICANT: Boesch, Jane E.
APPLICANT: Klom, Robert J.
TITLE OF INVENTION: METHOD FOR MODULATION OF CELL PHENOTYPE
FILE REFERENCE: 2648 34
CURRENT APPLICATION NUMBER: 09/09420060
CURRENT FILING DATE: 1999/10/18
NUMBER OF SEQ. ID NOS: 21
SOFTWARE: Patent In Release #1.0, Version #1.40
PRIORITY NO. 8
FILING DATE: 2001/04/11
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US 09 420 060 R

Query Match          R4.0K; Score 94; DB 19; Length 428;
Best Local Similarity 100.0K; Prod. No. 4.6e-06;
Matches 19; Conservatio 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSYRKILNLSND 22
DB 112 EILSRPSYRKILNLSND 140

RESULT 8
PRT 0302 27802 R
Sequence 2; Application PRT/030227802
GENERAL INFORMATION:
APPLICANT: The Rockefeller University
TITLE OF INVENTION: METHOD FOR CLASSIFICATION OF ANTI-ESTROGENIC DRUGS
FILE REFERENCE: 1161 609 228
CURRENT APPLICATION NUMBER: PRT/030227802
CURRENT FILING DATE: 2002/09/04
PRIORITY NO. 4
FILING DATE: 2001/06/14
LENGTH: 341
TYPE: PRT
ORGANISM: Homo sapiens
PRT 0302 27802 R

Query Match          R4.0K; Score 94; DB 13; Length 413;
Best Local Similarity 100.0K; Prod. No. 4.6e-06;
Matches 19; Conservatio 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSYRKILNLSND 22
DB 126 EILSRPSYRKILNLSND 144

RESULT 9
US 09 861 800 Z
Sequence 2; Application US/09861800
GENERAL INFORMATION:
APPLICANT: Hinkle, Steven H.
TITLE OF INVENTION: Methods and Compositions for Inhibiting
TITLE OF INVENTION: B-ZIP Transcription Factor Pathways
NUMBER OF SEQUENCES: 9

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Flagg, Ernst & Kurz
STREET: 1125 South Third Street, Suite 701
CITY: Omaha
STATE: Nebraska
COUNTRY: USA
ZIP: 68124
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,800
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NO. 6,210,880
FILING DATE: 18 MAR 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jondoe, Robert J.
REGISTRATION NUMBER: 43,915
REFERENCE/BOOKLET NUMBER: N1241 006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-398-9400
TELEFAX: 402-398-1984
INFORMATION FOR SEQ. ID NO: 2;
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-861-800 Z

Query Match          R4.0K; Score 94; DB 12; Length 441;
Best Local Similarity 100.0K; Prod. No. 4.6e-06;
Matches 19; Conservatio 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EILSRPSYRKILNLSND 22
DB 126 EILSRPSYRKILNLSND 144

RESULT 10
US 08 861-800A-2
Sequence 2; Application US/0881800A
GENERAL INFORMATION:
APPLICANT: Hinkle, Steven H.
TITLE OF INVENTION: Methods and Compositions for Inhibiting
TITLE OF INVENTION: B-ZIP Transcription Factor Pathways
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Flagg, Ernst & Kurz
STREET: 555 Thirteenth St., N.W., Suite 701 E
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,800A
FILING DATE: 24-JUN 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/210,880
FILING DATE: 18 MAR 1994

```



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1 GENERAL INFORMATION:
2 APPLICANT: Bojarski, Stephanie
3 APPLICANT: Iwaki, Hiroaki
4 APPLICANT: Iwaki, Hiroaki
5 APPLICANT: Iwaki, Hiroaki
6 APPLICANT: Iwaki, Hiroaki
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8 APPLICANT: Iwaki, Hiroaki
9 APPLICANT: Iwaki, Hiroaki
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100 APPLICANT: Iwaki, Hiroaki

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Quality Match: 90.2% Score: 89; DB: 22; Length: 93;
Best Local Similarity: 94.7%; Prod. No: 3,10-06;
Matches: 10; Conservat: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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27 4 ELLSRPSTYKTLNLSND 22
db 60 ELLSRPSTYKTLNLSND 22

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Search completed: January 2, 2003, 12:45:21
CPU Time: 1.04 secs

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RESULT 2
US-09-215-098-5
: SEQUENCE 5, Application US/09215098
: Patent No. 6194642
: GENERAL INFORMATION:
: APPLICANT: LEBRON, JEFFERY M
: TITLE OF INVENTION: PLACENTAL CIRCULATORY PATHWAY IN TRANSFERRING MOLE EXPRESSING A
: TITLE OF INVENTION: CHIMERIC HEMATOPHAGOCYTIC TRANSCRIPTION FACTOR IN THE
: TITLE OF INVENTION: HEART
: FILE REFERENCE: 9189-4
: CURRENT APPLICATION NUMBER: US/09/215,098
: CURRENT FILING DATE: 1998-12-18
: PRIOR APPLICATION NUMBER: 60/066,011
: PRIOR FILING DATE: 1997-12-18
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 5
: LENGTH: 427
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-215-098-5

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Query Match 81.8% Score 93 DP 41 Length 427
Best Local Similarity 100.0% Pred. No. 4.3e-07
Matches 14 Conservative 0 Mismatches 0 Indels 0 Gaps 0

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4 EILSRPSYRKILNDL 22
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112 EILSRPSYRKILNDL 140

RESULT 4
US-09-252-658-6
: SEQUENCE 6, Application US/09252658
: Patent No. 6251667
: GENERAL INFORMATION:
: APPLICANT: HABERER, JOHN F.
: APPLICANT: BOEFLER, JAMES P.
: TITLE OF INVENTION: A CAMP-RESPONSIVE TRANSCRIPTIONAL
: TITLE OF INVENTION: BRANCHED BINDING PROTEIN
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STEPHEN KESSLER, GOLDSTEIN & FOX P L L C
: STREET: 1100 NEW YORK AVE , NW, STE. 600
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/252,658
: FILING DATE: HEREWITH
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/684,965
: FILING DATE: 22-MAY-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US99/95234
: FILING DATE: 20-NOV-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/672,920
: FILING DATE: 18-NOV-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Gimbalaz, Michele A
: REGISTRATION NUMBER: 31,851
: REFERENCE/DOCKET NUMBER: 0409 156002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)371-2600
: TELEFAX: (202)371-2540

```

```

: INFORMATION FOR SEQ ID NO 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 427 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US 09-252-658-6

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Query Match 81.8% Score 93 DP 41 Length 427
Best Local Similarity 100.0% Pred. No. 4.4e-07
Matches 14 Conservative 0 Mismatches 0 Indels 0 Gaps 0

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4 EILSRPSYRKILNDL 22
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112 EILSRPSYRKILNDL 140

RESULT 4
US-08-442-181-1
: SEQUENCE 1, Application US/08442181
: Patent No. 5814459
: GENERAL INFORMATION:
: APPLICANT: MONTAGNY, Marc R.
: TITLE OF INVENTION: PROTEIN-SPECIFIC TRANSCRIPTION FACTOR
: TITLE OF INVENTION: ANTIBODIES
: NUMBER OF SEQUENCES: 1
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Spensley Horn Jubas & Lubitz
: STREET: 1890 Century Park East, Suite 500
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90067
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 02/08,442,181
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/4016,839
: FILING DATE: 02-FEB-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Welherell, Jr. Ph.D., John R.
: REGISTRATION NUMBER: 31,678
: REFERENCE/DOCKET NUMBER: FD-2217
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-455-5100
: TELEFAX: 619-455-5110
: INFORMATION FOR SEQ ID NO 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 14 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1..14
US-08-442-181-1

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Query Match 83.3% Score 70 DP 25 Length 14
Best Local Similarity 100.0% Pred. No. 5.4e-05
Matches 14 Conservative 0 Mismatches 0 Indels 0 Gaps 0

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6 LSRKPSYRKILNDL 19
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1 LSRKPSYRKILNDL 14

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1 TELEFAX: (202) 371-2540
2 INFORMATION FOR SEQ ID NO: 17:
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 1099 amino acids
5 TYPE: amino acid
6 topology: linear
7
8 US 09 665 574 17
9
10 Query Match
11 Best Local Similarity 42.4% Score 47: 108 4: Length 1099:
12 Matches 9: Conservation 2: Mismatches 0: Gaps 0:
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1 COMPUTER: IBM PC compatible  
 2 OPERATING SYSTEM: PC-DOS/MS-DOS  
 3 SOFTWARE: Patent in Release #1.3, Version #1.30  
 4 CURRENT APPLICATION DATA:  
 5 APPLICATION NUMBER: US/09/004,289  
 6 FILING DATE:  
 7 CLASSIFICATION:  
 8 PRIOR APPLICATION DATA:  
 9 APPLICATION NUMBER: US/08/457,598  
 10 FILING DATE: 15-DEC-1994  
 11 ATTORNEY/AGENT INFORMATION:  
 12 NAME: Bailo, Lisa A.  
 13 REGISTRATION NUMBER: 48,447  
 14 REFERENCE NUMBER: 07265-033601  
 15 TELECOMMUNICATION INFORMATION:  
 16 TELEPHONE: 619/678 5090  
 17 TELEFAX: 619/678-5099  
 18 INFORMATION FOR SEQ ID NO: 11:  
 19 SEQUENCE CHARACTERISTICS:  
 20 LENGTH: 1100 amino acids  
 21 TYPE: amino acid  
 22 STRANDEDNESS: Not relevant  
 23 TOPOLOGY: linear  
 24 MOLECULE TYPE: protein  
 25 US-09-004,289-11  
 26  
 27 Query Match 42.3% Score 47, DB 2, Length 1100,  
 28 Best Local Similarity 69.2%, Prod. No. 32,  
 29 Matches 9, Conservative 2, Mismatches 2, Indels 0, Gaps 0,  
 30  
 31 QY 8 KPSYRKILNLS 20  
 32 IIILIIIIII  
 33 DB 762 KRSPRALRLN 774

34  
 35 RESULT 14  
 36 PCT-US95-10435-11  
 37 Sequence 2, Application: PCT/US95/01649  
 38 GENERAL INFORMATION:  
 39 APPLICANT: The Johns Hopkins University School of Medicine  
 40 TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3  
 41 NUMBER OF SEQUENCES: 12  
 42 CORRESPONDENCE ADDRESS:  
 43 ADDRESSEE: Fish & Richardson P.C.  
 44 STREET: 420 Executive Square, Suite 1400  
 45 CITY: La Jolla  
 46 STATE: CA  
 47 COUNTRY: USA  
 48 ZIP: 92037  
 49 COMPUTER READABLE FORM:  
 50 MEDIUM TYPE: Floppy disk  
 51 COMPUTER: IBM PC compatible  
 52 OPERATING SYSTEM: PC-DOS/MS-DOS  
 53 SOFTWARE: Patent in Release #1.0, Version #1.30  
 54 CURRENT APPLICATION DATA:  
 55 APPLICATION NUMBER: PCT/US95/01645  
 56 FILING DATE: 15 DEC 1995  
 57 CLASSIFICATION:  
 58 ATTORNEY/AGENT INFORMATION:  
 59 NAME: Bailo, Lisa A.  
 60 REGISTRATION NUMBER: 38,347  
 61 REFERENCE NUMBER: 07265-033601  
 62 TELECOMMUNICATION INFORMATION:  
 63 TELEPHONE: 619/678 5070  
 64 TELEFAX: 619/678 5099  
 65 INFORMATION FOR SEQ ID NO: 11:  
 66 SEQUENCE CHARACTERISTICS:  
 67 LENGTH: 1100 amino acids  
 68 TYPE: amino acid  
 69 STRANDEDNESS: not relevant  
 70 TOPOLOGY: linear  
 71 MOLECULE TYPE: protein  
 72 PCT-US95-10435-11

73 Query Match 42.3% Score 47, DB 5, Length 1100,  
 74 Best Local Similarity 69.2%, Prod. No. 42,  
 75 Matches 9, Conservative 2, Mismatches 2, Indels 0, Gaps 0,  
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 78 IIILIIIIII  
 79 DB 762 KRSPRALRLN 774  
 80  
 81 RESULT 15  
 82 PCT-US95-08354A-2  
 83 Sequence 2, Application: PCT/US95/08354A  
 84 GENERAL INFORMATION:  
 85 APPLICANT: Temple University - of The  
 86 ATTORNEY/AGENT INFORMATION:  
 87 TITLE OF INVENTION: JAK2 PROTEIN TYROSINE  
 88 TITLE OF INVENTION: KINASE AND RNA ENZYME THE SAME  
 89 NUMBER OF SEQUENCES: 9  
 90 CORRESPONDENCE ADDRESS:  
 91 ADDRESSEE: Seidel, Gonda, Lavorata  
 92 ADDRESSEE: & Monaco, P.C.  
 93 STREET: Suite 1800, Two Penn Center  
 94 CITY: Philadelphia  
 95 STATE: Pennsylvania  
 96 COUNTRY: U.S.A.  
 97 ZIP: 19102  
 98 COMPUTER READABLE FORM:  
 99 MEDIUM TYPE: diskette, 3.50 inch, 720 Kb  
 100 COMPUTER: IBM PS/2  
 101 OPERATING SYSTEM: MS-DOS  
 102 SOFTWARE: Wordperfect 5.1  
 103 CURRENT APPLICATION DATA:  
 104 APPLICATION NUMBER: PCT/US95/08354A  
 105 FILING DATE:  
 106 CLASSIFICATION:  
 107 PRIOR APPLICATION DATA:  
 108 APPLICATION NUMBER: 39,372,468  
 109 FILING DATE: 8 July 1994  
 110 ATTORNEY/AGENT INFORMATION:  
 111 NAME: Monaco, Daniel A.  
 112 REGISTRATION NUMBER: 30,480  
 113 REFERENCE NUMBER: 6056-203 PC  
 114 TELECOMMUNICATION INFORMATION:  
 115 TELEPHONE: (215) 568-8384  
 116 TELEFAX: (215) 568-5549  
 117 INFORMATION FOR SEQ ID NO: 2:  
 118 SEQUENCE CHARACTERISTICS:  
 119 LENGTH: 1299 amino acids  
 120 TYPE: amino acid  
 121 STRANDEDNESS: single stranded  
 122 TOPOLOGY: linear  
 123 PCT-US95-08354A-2

124 Query Match 42.3% Score 47, DB 5, Length 1299,  
 125 Best Local Similarity 69.2%, Prod. No. 48,  
 126 Matches 9, Conservative 2, Mismatches 2, Indels 0, Gaps 0,  
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 128 QY 8 KPSYRKILNLS 20  
 129 IIILIIIIII  
 130 DB 977 KRSPRALRLN 989  
 131  
 132 Search completed: January 2, 2003, 12:29:45  
 133 Job time: 13 secs



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: PRIOR APPLICATION NUMBER: US/09/951-902-1
: PRIOR FILING DATE: 2001-01-03
: PRIOR APPLICATION NUMBER: 60/206,115
: PRIOR FILING DATE: 2000-05-22
: PRIOR APPLICATION NUMBER: 60/174,308
: PRIOR FILING DATE: 2000-01-03
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic
: NAME/KEY: misc_feature
: LOCATION: (11)..(11)
: OTHER INFORMATION: Ser residue 11 is phosphorylated.
US-09-951-902-1

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Query Match          45.0%; Score 50; DP 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 EILSRPSPYR 13
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Db 4 EILSRPSPYR 13

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RESULT 4
US-09-951-902-2
: Sequence 2; Application US/09/951-902
: Patent No. US20020147146A1
: GENERAL INFORMATION:
: APPLICANT: ELIAR-FINKELMAN, Hagit
: TITLE OF INVENTION: GLYCOSYL SYNTHASE KINASE-3 INHIBITORS
: FILE REFERENCE: ELIAR-FINKELMAN, Hagit
: CURRENT FILING DATE: 2001-09-14
: PRIOR APPLICATION NUMBER: 60/174,308
: PRIOR FILING DATE: 2001-01-03
: PRIOR APPLICATION NUMBER: 60/206,115
: PRIOR FILING DATE: 2000-05-22
: PRIOR APPLICATION NUMBER: 60/174,308
: PRIOR FILING DATE: 2000-01-03
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic
US-09-951-902-2

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Query Match          45.0%; Score 50; DP 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 EILSRPSPYR 13
   111111111
Db 4 EILSRPSPYR 13

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RESULT 4
US-09-951-902-5
: Sequence 5; Application US/09/951-902
: Patent No. US20020147146A1
: GENERAL INFORMATION:
: APPLICANT: ELIAR-FINKELMAN, Hagit
: TITLE OF INVENTION: GLYCOSYL SYNTHASE KINASE-3 INHIBITORS
: FILE REFERENCE: ELIAR-FINKELMAN, Hagit
: CURRENT FILING DATE: 2001-09-14
: PRIOR APPLICATION NUMBER: 60/206,115
: PRIOR FILING DATE: 2000-05-22
: PRIOR APPLICATION NUMBER: 60/174,308
: PRIOR FILING DATE: 2000-01-03
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic
US-09-951-902-5

```

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: PRIOR APPLICATION NUMBER: US/09/951-902-3
: PRIOR FILING DATE: 2001-01-03
: PRIOR APPLICATION NUMBER: 60/206,115
: PRIOR FILING DATE: 2000-05-22
: PRIOR APPLICATION NUMBER: 60/174,308
: PRIOR FILING DATE: 2000-01-03
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic
: NAME/KEY: misc_feature
: LOCATION: (11)..(11)
: OTHER INFORMATION: Ser residue 11 is phosphorylated.
US-09-951-902-3

```

```

Query Match          42.3%; Score 47; DP 10; Length 13;
Best Local Similarity 90.0%; Pred. No. 0.093;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 EILSRPSPYR 13
   111111111
Db 4 EILSRPSPYR 13

```

```

RESULT 5
US-09-951-902-3
: Sequence 3; Application US/09/951-902
: Patent No. US20020147146A1
: GENERAL INFORMATION:
: APPLICANT: ELIAR-FINKELMAN, Hagit
: TITLE OF INVENTION: GLYCOSYL SYNTHASE KINASE-3 INHIBITORS
: FILE REFERENCE: ELIAR-FINKELMAN, Hagit
: CURRENT FILING DATE: 2001-09-14
: PRIOR APPLICATION NUMBER: 60/174,308
: PRIOR FILING DATE: 2001-01-03
: PRIOR APPLICATION NUMBER: 60/206,115
: PRIOR FILING DATE: 2000-05-22
: PRIOR APPLICATION NUMBER: 60/174,308
: PRIOR FILING DATE: 2000-01-03
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 3
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic
: NAME/KEY: misc_feature
: LOCATION: (7)..(7)
: OTHER INFORMATION: Ser residue 7 is phosphorylated.
US-09-951-902-3

```

```

Query Match          40.5%; Score 45; DP 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.8e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 ILSRPSPYR 13
   111111111
Db 1 ILSRPSPYR 9

```

```

RESULT 6
US-09-951-902-12
: Sequence 12; Application US/09/951-902
: Patent No. US20020147146A1
: GENERAL INFORMATION:
: APPLICANT: ELIAR-FINKELMAN, Hagit
: TITLE OF INVENTION: GLYCOSYL SYNTHASE KINASE-3 INHIBITORS
: FILE REFERENCE: ELIAR-FINKELMAN, Hagit
: CURRENT FILING DATE: 2001-09-14
: PRIOR APPLICATION NUMBER: 60/206,115
: PRIOR FILING DATE: 2000-05-22
: PRIOR APPLICATION NUMBER: 60/174,308
: PRIOR FILING DATE: 2000-01-03
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 12
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic
US-09-951-902-12

```



: CURRENT FILING DATE: 2001-03-21  
 : PRIOR APPLICATION NUMBER: 60/191,078  
 : PRIOR FILING DATE: 2000-03-21  
 : PRIOR APPLICATION NUMBER: 60/236,919  
 : PRIOR FILING DATE: 2000-05-23  
 : PRIOR APPLICATION NUMBER: 60/267,727  
 : PRIOR FILING DATE: 2000-05-26  
 : PRIOR APPLICATION NUMBER: 60/242,578  
 : PRIOR FILING DATE: 2000-10-23  
 : PRIOR APPLICATION NUMBER: 60/273,625  
 : PRIOR FILING DATE: 2000-11-27  
 : PRIOR APPLICATION NUMBER: 60/327,731  
 : PRIOR FILING DATE: 2000-12-30  
 : PRIOR APPLICATION NUMBER: 60/264,308  
 : PRIOR FILING DATE: 2001-02-16  
 : NUMBER OF SEQ ID NOS: 14110  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 11305  
 : LENGTH: 577  
 : TYPE: PRT  
 : ORGANISM: Helicobacter pylori  
 US-09-815-242-11305

Query Match 38.7%; Score 43; DB 10; Length 577;  
 Best Local Similarity 42.1%; Pred. No. 33;  
 Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 4 ELRSRPSYKIIINQSSD 22  
 DB 173 RLNTQSAKRIISQGLD 191

## RESULT 11

US-09-817-514A-6  
 : Sequence 6; Application US/99817514A  
 : Patent No. US20020078478A1  
 : GENERAL INFORMATION:  
 : APPLICANT: French-Constant, Richard  
 : APPLICANT: Bowen, David  
 : APPLICANT: Rocheleau, Thomas  
 : APPLICANT: Waterfield, Nicholas  
 : TITLE OF INVENTION: DNA SEQUENCES FROM PHOTOBACULUS LUMINESCENS  
 : FILE REFERENCE: 61645  
 : CURRENT APPLICATION NUMBER: US/99/817,514A  
 : CURRENT FILING DATE: 2000-03-26  
 : PRIOR APPLICATION NUMBER: US 60/191806  
 : PRIOR FILING DATE: 2000-03-24  
 : NUMBER OF SEQ ID NOS: 8  
 : SOFTWARE: Patent In version 3.0  
 : SEQ ID NO 6  
 : LENGTH: 915  
 : TYPE: PRT  
 : ORGANISM: Photobaculus luminescens  
 US-09-817-514A-6

Query Match 48.7%; Score 43; DB 10; Length 915;  
 Best Local Similarity 60.0%; Pred. No. 57;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 ILSRPSYKIIINQ 15  
 DB 400 IIRPSIAKVIQDL 314

## RESULT 12

US-09-801-368-72  
 : Sequence 72; Application US/9981368  
 : Patent No. US20020128250A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Busby, Robert  
 : APPLICANT: Calli, Brian  
 : APPLICANT: Hecht, Peter  
 : APPLICANT: Holtzman, Doug

: APPLICANT: Madden, Kevin  
 : APPLICANT: Maxon, Mary  
 : APPLICANT: Milne, Todd  
 : APPLICANT: N. 552020128250Alman, Thea  
 : APPLICANT: Royer, John  
 : APPLICANT: Salama, Sofia  
 : APPLICANT: Sherman, Amir  
 : APPLICANT: Silva, Jeff  
 : APPLICANT: Summers, Eric  
 : TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
 : FILE REFERENCE: 199272,147  
 : CURRENT APPLICATION NUMBER: US 60/160,658  
 : CURRENT FILING DATE: 2001-03-07  
 : PRIOR APPLICATION NUMBER: US 60/487,558  
 : PRIOR FILING DATE: 2000-01-19  
 : PRIOR APPLICATION NUMBER: US 60/160,587  
 : PRIOR FILING DATE: 1999-10-20  
 : NUMBER OF SEQ ID NOS: 440  
 : SOFTWARE: Patent In version 3.0  
 : SEQ ID NO 72  
 : LENGTH: 1131  
 : TYPE: PRT  
 : ORGANISM: Saccharomyces cerevisiae  
 US 09 801 368 72

Query Match 39.7%; Score 43; DB 10; Length 1131;  
 Best Local Similarity 50.0%; Pred. No. 73;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 TSSEIIISRRPSYKIIINQ 18  
 DB 997 SSSEIOANYDKYIKVLINQ 1014

## RESULT 13

US-10-014-485A-115  
 : Sequence 115; Application US/10014485A  
 : Patent No. US20020168684A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Cell Signaling Technology, Inc.  
 : APPLICANT: COMB, Michael J.  
 : APPLICANT: ZHANG, Hui  
 : APPLICANT: TAN, Yi  
 : TITLE OF INVENTION: PROTECTION OF BPTIF SPECIFIC AND CONTEXT INDEPENDENT ANTIBODIES  
 : FILE REFERENCE: CST-138 CIP2  
 : CURRENT APPLICATION NUMBER: US/10/014,485A  
 : CURRENT FILING DATE: 2002-04-18  
 : PRIOR APPLICATION NUMBER: US 65/148,712  
 : PRIOR FILING DATE: 1998-09-04  
 : PRIOR APPLICATION NUMBER: US 09/535,364  
 : PRIOR FILING DATE: 2000-04-24  
 : NUMBER OF SEQ ID NOS: 145  
 : SOFTWARE: Patent In version 3.1  
 : SEQ ID NO 115  
 : LENGTH: 8  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 : FEATURE:  
 : NAME/KEY: MOD\_RES  
 : LOCATION: (5)..(5)  
 : OTHER INFORMATION: PHOSPHORYLATION: serine at position 5 is phosphorylated  
 US-10-014-485A-115

Query Match 37.8%; Score 42; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9; Indels 0; Gaps 0;

QY 7 SRPSYK 14  
 DB 1 SRPSYK 8



1. The first part of the document discusses the importance of maintaining accurate records of all transactions and the role of the accounting system in providing reliable financial information. It emphasizes the need for transparency and accountability in financial reporting.

2. The second part of the document outlines the various methods used to collect and analyze financial data, including the use of statistical techniques and the application of mathematical models. It highlights the importance of using appropriate methods to ensure the accuracy and reliability of the results.

3. The third part of the document discusses the challenges faced by organizations in managing their financial resources and the role of the accounting system in addressing these challenges. It emphasizes the need for effective financial management and the importance of using the accounting system to monitor and control financial performance.

4. The fourth part of the document discusses the role of the accounting system in providing financial information to management and the importance of using this information to make informed decisions. It emphasizes the need for accurate and timely financial information and the role of the accounting system in providing this information.

5. The fifth part of the document discusses the role of the accounting system in providing financial information to external stakeholders and the importance of using this information to make informed decisions. It emphasizes the need for accurate and timely financial information and the role of the accounting system in providing this information.

6. The sixth part of the document discusses the role of the accounting system in providing financial information to the public and the importance of using this information to make informed decisions. It emphasizes the need for accurate and timely financial information and the role of the accounting system in providing this information.

7. The seventh part of the document discusses the role of the accounting system in providing financial information to the government and the importance of using this information to make informed decisions. It emphasizes the need for accurate and timely financial information and the role of the accounting system in providing this information.

8. The eighth part of the document discusses the role of the accounting system in providing financial information to the media and the importance of using this information to make informed decisions. It emphasizes the need for accurate and timely financial information and the role of the accounting system in providing this information.

9. The ninth part of the document discusses the role of the accounting system in providing financial information to the public and the importance of using this information to make informed decisions. It emphasizes the need for accurate and timely financial information and the role of the accounting system in providing this information.

10. The tenth part of the document discusses the role of the accounting system in providing financial information to the public and the importance of using this information to make informed decisions. It emphasizes the need for accurate and timely financial information and the role of the accounting system in providing this information.













XX Disclosure: Page 16; 34pp; English.

XX The present invention relates to a biomolecular substrate,

XX comprising a core molecular backbone, a fluorescent dye and a

XX second dye. The dye changes state if the biomolecular substrate

XX is covalently modified. The invention is useful for assaying

XX covalent biomolecular modification in a sample. For example, it

XX is useful for assaying protein kinase activity.

XX Sequence 24 AA:

Query Match 68.5%; Score 76; Pos 22; Length 24;

Best Local Similarity 93.8%; Pred. No. 5.2e-05;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 ELISRRPSYRKILNQL 19

DB 7 ELISRRPSYRKILNQL 22

RESULT 1J

AAE00656

1D AAE00656 standard; peptide; 22 AA.

XX AAE00656;

XX AAE00656;

XX 02 JUL 2001 (first entry)

XX Human activating transcription factor-1 (ATF-1) protein.

XX Human; cyclic adenosine mono phosphate; cell phenotype modulator; CREB;

XX cAMP responsive element binding protein; antidiabetic; cytostatic;

XX neuroprotective; neotropic; osteoprotegic; antihypertensive; antidiabetic;

XX antiatherosclerotic; vasoregulatory; neuroprotective; antidepressant;

XX cardiac; hypotensive; obesity; cardiovascular disease; cardiomyopathy;

XX congestive heart failure; macrovascular disease; polymathy hypotension;

XX acute myocardial infarction; stroke; peripheral vascular disease;

XX post angioplasty restenosis; heart failure; neurodegenerative disease;

XX Alzheimer's disease; Parkinson's disease; spinal transection;

XX acute neuronal ischaemia; tumour neovascularisation; ATF-1;

XX activating transcription factor-1.

XX Homo sapiens.

XX W-200129062-A2.

XX 26-APR-2001.

XX 12-OCT-2000; 2000W0-US28316.

XX 18-OCT-1999; 99US-0420060.

XX (NYE ) UNIV TECHNOLOGY CORP.

XX (NYE ) NAT PHARM MEDICAL & PHARM CORP.

XX (USGO ) US DEPT VETERANS AFFAIRS.

XX Kouschik, Klemm 101;

XX W-2001-290991/30.

XX N PSDB; AAE00656.

XX Modulating cell phenotype in a patient having or risk of developing a

XX disease or condition associated with dysregulation of cellular phenotype,

XX comprises administering nucleic acid encoding cyclic AMP responsive

XX element binding protein.

XX Claim 5, Page 154 155; 156pp; English.

XX The patent discloses a method for modulating the phenotype of a target

XX cell population in a patient, which has or is at risk of developing a

XX disease or condition associated with dysregulation of cellular

XX phenotype. The method involves the administration of a composition

XX containing a recombinant nucleic acid molecule (rNA) encoding a cyclic-

XX AMP responsive element binding (cAMP) protein having CREB biological

XX activity to a patient, such that the cAMP protein is expressed in

XX target cells, and is sufficient to modulate the phenotype of the

XX target cells. CREB protein is a transcription factor necessary and

XX sufficient to induce a modulation in cell phenotype and to induce cell

XX The present invention relates to a biomolecular substrate,

XX comprising a core molecular backbone, a fluorescent dye and a

XX second dye. The dye changes state if the biomolecular substrate

XX is covalently modified. The invention is useful for assaying

XX covalent biomolecular modification in a sample. For example, it

XX is useful for assaying protein kinase activity.

XX Sequence 24 AA:

Query Match 67.6%; Score 75; Pos 22; Length 22;

Best Local Similarity 93.8%; Pred. No. 6.8e-05;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 ELISRRPSYRKILNQL 19

DB 7 ELISRRPSYRKILNQL 22

RESULT 1J

AAE00656

1D AAE00656 standard; peptide; 271 AA.

XX AAE00656;

XX AAE00656;

XX 02 JUL 2001 (first entry)

XX Human activating transcription factor-1 (ATF-1) protein.

XX Human; cyclic adenosine mono phosphate; cell phenotype modulator; CREB;

XX cAMP responsive element binding protein; antidiabetic; cytostatic;

XX neuroprotective; neotropic; osteoprotegic; antihypertensive; antidiabetic;

XX antiatherosclerotic; vasoregulatory; neuroprotective; antidepressant;

XX cardiac; hypotensive; obesity; cardiovascular disease; cardiomyopathy;

XX congestive heart failure; macrovascular disease; polymathy hypotension;

XX acute myocardial infarction; stroke; peripheral vascular disease;

XX post angioplasty restenosis; heart failure; neurodegenerative disease;

XX Alzheimer's disease; Parkinson's disease; spinal transection;

XX acute neuronal ischaemia; tumour neovascularisation; ATF-1;

XX activating transcription factor-1.

XX Homo sapiens.

XX W-200129062-A2.

XX 26-APR-2001.

XX 12-OCT-2000; 2000W0-US28316.

XX 18-OCT-1999; 99US-0420060.

XX (NYE ) UNIV TECHNOLOGY CORP.

XX (NYE ) NAT PHARM MEDICAL & PHARM CORP.

XX (USGO ) US DEPT VETERANS AFFAIRS.

XX Kouschik, Klemm 101;

XX W-2001-290991/30.

XX N PSDB; AAE00656.

XX Modulating cell phenotype in a patient having or risk of developing a

XX disease or condition associated with dysregulation of cellular phenotype,

XX comprises administering nucleic acid encoding cyclic AMP responsive

XX element binding protein.

XX Claim 5, Page 154 155; 156pp; English.

XX The patent discloses a method for modulating the phenotype of a target

XX cell population in a patient, which has or is at risk of developing a

XX disease or condition associated with dysregulation of cellular

XX phenotype. The method involves the administration of a composition

XX containing a recombinant nucleic acid molecule (rNA) encoding a cyclic-

XX AMP responsive element binding (cAMP) protein having CREB biological

XX activity to a patient, such that the cAMP protein is expressed in

XX target cells, and is sufficient to modulate the phenotype of the

XX target cells. CREB protein is a transcription factor necessary and

XX sufficient to induce a modulation in cell phenotype and to induce cell









XX PS Disclosure: Page 38; 45pp; Japanese.

XX CC this sequence represents a leucine phosphorylation region.

XX CC the invention relates to a monitor protein (1) for measuring

XX CC phosphorylation of a protein. (1) comprises a protein containing a

XX CC phosphorylation region and a characteristically variable region, where

XX CC characteristics vary due to a change in the stereostructure. It is

XX CC conveniently applicable for use in vivo determination without needing

XX CC radioisotopes. (1) is useful for the measurement of phosphorylation of

XX CC protein, and for in vivo determination without needing radioisotopes

XX CC e.g. in studying phosphorylation reaction and screening kinases and

XX CC promoters and inhibitors of phosphorylation

SQ Sequence 24 AA:

Query Match 100.0%; Score 100; PP 21; Length 23;

Best Local Similarity 100.0%; Pred. No. 3.5e-10;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLRRASLTGCHAVRAIGRLSST 23

IB 1 TSLRRASLTGCHAVRAIGRLSST 23

RESULT 2

AAW74294

ID AAW74294 standard; Peptide, 26 AA.

AC AAW74294

DT 08-FEB-1999 (first entry)

DE Calmodulin-binding peptide.

XX KW Calmodulin-binding peptide; ligand detection; green fluorescent protein;

XX FW ligand-dependent fluorescent resonant energy transfer; FRET.

XX OS Synthetic.

XX W0949279 A1.

XX 29-05-1999.

XX 23-APR-1998; 5860-0508109.

XX 24-APR-1997; 9795-0942322.

XX (GFP ) UNIV ROCHESTER.

XX Persechini A;

XX WPI: 1998-584821/49.

XX New complex of two green fluorescent proteins connected by

XX ligand-binding peptide useful for, e.g. measuring levels of

XX specific ligands in cells, monitoring changes, and for identifying

XX agents with ligand binding activity

XX Claim 4; Page 25; 55pp; English.

XX CC This sequence represents a calmodulin-binding peptide, and is used as a

XX CC primary ligand binding peptide in the method of the invention. The method

XX CC is for monitoring the amount of a primary ligand (1) in a cell by forming

XX CC a green fluorescent protein (GFP) complex (A) consisting of: (i) a first

XX CC GFP; (ii) a (1)-binding peptide attached to the first GFP at its

XX CC N-terminus; and (iii) a second GFP attached to the C-terminus of the

XX CC (1)-binding peptide, where the first GFP is excited at wavelength W1 and

XX CC emits fluorescence at wavelength W2, while the second GFP is excited at

XX CC W2 and emits at wavelength W3. The complex is introduced into a cell, and

XX CC the base amount of fluorescent emission at W3 when the cell is excited at

XX CC W1 is measured. The fluorescence emission over time recorded at W3, when

XX CC excited at W1 is also measured, and is then compared with the base

XX CC emission. Any change in emission indicates a change in the amount of (1).

XX CC the method is used to determine maximal and resting levels of (1) in

XX CC different cell types and at different stages of the cell cycle; also

XX CC spatio-temporal changes in (1)-binding activity during cellular events.

XX CC It may be modified to determine the amount of a secondary ligand in a

XX CC cell. The method is based on ligand dependent fluorescent resonant energy

XX CC transfer (FRET) between the two GFP.

SQ Sequence 26 AA:

Query Match 59.7%; Score 76; PP 19; Length 26;

Best Local Similarity 78.3%; Pred. No. 5.6e-05;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TSLRRASLTGCHAVRAIGRLSST 24

IB 2 TSSPPFWNCTCHAVRAIGRLSST 24

RESULT 3

ABB83068

ID ABB83068 standard; Peptide; 21 AA.

XX AC ABB83068;

XX 05-SEP-2002 (first entry)

XX DE M23 segment of smooth muscle myosin light chain kinase.

XX KW Biosensor protein; green fluorescent protein; GFP; calmodulin sensor;

XX FW fluorescence; smooth muscle; myosin light chain kinase.

XX OS Synthetic.

XX EP1209167-A1.

XX 29-MAY-2002.

XX 21-NOV-2001; 2001FP-0127775.

XX 22-NOV-2000; 2000JP-0356047.

XX (GKAL ) OKAZAKI NAT RES INST.

XX Nakai J;

XX WPI: 2000-341378/50.

XX N-PSDB: ABB83906.

XX Producing a biosensor protein capable of regulating fluorescence

XX property of green fluorescence protein comprises predicting an amino acid

XX residue that affects fluorescence, and fusing with a functional

XX molecule.

XX Example 1; Page 25; 49pp; English.

XX CC The invention relates to producing a biosensor protein capable of

XX CC regulating a fluorescence property of green fluorescent protein (GFP).

XX CC This comprises predicting an amino acid affecting a fluorescence property

XX CC of GFP, producing fusion proteins with GFP and functional molecule(s),

XX CC reacting with a factor affecting the conformation of the functional

XX CC molecules and screening a fusion protein exhibiting a change in the

XX CC fluorescence property. The method is useful for producing a biosensor

XX CC protein (especially a calmodulin-sensing biosensor protein) capable of

XX CC regulating a fluorescence property of GFP. The method of producing

XX CC proteins with a unique structure produces proteins with a high

XX CC sensitivity, unlike prior art methods producing proteins with low

XX CC sensitivity. A specific detection device is not needed. The current

XX CC sequence represents M23 segment of smooth muscle myosin light chain

XX CC kinase amino acid sequence. This is used in the context of the invention

XX CC as a functional molecule.

SQ Sequence 21 AA:



US	McIntyre is gallopavo.
XX	
IN	W0200071565-A2.
XX	
PD	40-NOV-2000.
XX	
PF	17 MAY-2000; 2000W0-US13684.
XX	
DR	21-MAY-1999; 99US-0416919.
PF	21-MAY-1999; 99US-0416920.
XX	
PA	(RENC ) UNIV CALIFORNIA.
XX	
PI	Islen RV, Baird GA;
XX	
DR	WPI; 2001 032017/04.
XX	
PT	Novel fluorescent proteins comprising a sensor protein inserted into
PI	them, useful for measuring the response of a subject biological,
XX	chemical, electrical or physiological parameter in vivo or in vitro.
XX	
PS	Disclosure; Page 32, 94pp, English.
XX	
QC	The present sequence is a calmodulin binding domain peptide used in the
QC	construction of a fluorescent protein indicator. The indicator comprises
QC	a sensor polypeptide that is responsive to a specific biological,
QC	electrical or physiological parameter, and a fluorescence protein
QC	functional group. The sensor polypeptide is operatively inserted into the
QC	fluorescent moiety. The fluorescent indicator is useful for detecting the
QC	presence of a response inducing member in a sample. The method involves
QC	contacting the sample with the indicator and detecting a change in
QC	fluorescence, in which a change is indicative of the effect of the
QC	parameter on the sensor polypeptide. The novel fluorescent proteins are
QC	advantageous due to their reduced size as compared to the FRET
QC	(fluorescence resonance energy transfer)-based sensors.
XX	
SQ	Sequence 20 AA;
XX	

PR	23-0CT-1998;	98US 0105471.
PR	22-0CT-1999;	99US-042862.
XX	(AMGE) - AMGEN INC.	
PA	Ferre U., Lin C., Cheetham J., Boone IC;	
PL	WPI; 2900 454/24730.	
LF		
XX		
PT	Novel composition of matter comprising an Fe domain and	
PT	pharmacologically active peptides, useful for treating cancer and	
PL	autoimmune diseases .	
XX		
PS	Claim 39; Page 254; 608pp; English.	
XX		
CC	The present invention describes composition of matter (i) comprising an	
CC	Fe domain, pharmacologically active peptides, and linkers, where (1) is:	
CC	(X1)a-P3-(X2)b, where, P1 = an Fe domain, X1 and X2 = are each	
CC	independently selected from: (I), F1, (II), F1, (III), F1, (IV), F1,	
CC	(V), F1, (VI), F1, (VII), F1, (VIII), F1, (IX), F1, (X), F1, (XI), F1,	
CC	where P1, P2, P3, and P4 = are each independently sequences of	
CC	pharmacologically active peptides, L1, L2, L3, and L4 = are each	
CC	independently linkers, and a, b, c, d, e, and f = are each independently	
CC	0 or 1, provided that at least 1 of a and b is 1. The composition can	
CC	have cytostatic, antiasthmatic, thrombolytic and immunosuppressive	
CC	activities. BMS, receptors and test cells from the present invention can	
CC	be used for producing pharmaceutical compositions. The compositions are	
CC	useful for treating cancer, asthma, rheumatoid arthritis, autoimmune diseases.	
CC	The use of an Fe domain (rather than a Fab domain) can provide a longer	
CC	half life or inactivate functions such as Fe receptor binding, protein	
CC	A binding, complement fixation, and possibly placental transfer. AAA69443	
CC	to AAA69556 and AAA69557 to AAA69559 represent nucleotide and amino acid	
CC	sequences used in the exemplification of the present invention.	
XX		
SQ	Sequence 18 AA:	
	Query Match 57.8%, Score 63, DB 21; Length 18;	
	Best Local Similarity 100.0%; Pred. No. 0.0041;	
	Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
27	10 TCBAVPAICGLSS 22	
DB	6 TCBAVPAICGLSS 18	
RESULT 8		
ABW73197		
ID	ABW73197 standard; Peptide; 18 AA.	
AC	ABW73197;	
XX		
XX	05-APR-2002 (first entry)	
DE	Calmmodulin antagonist peptide SEQ ID NO:175.	
XX		
KW	Modified peptide; mimetic; Fe domain; fusion; immunoglobulin G; IgG;	
KW	erythropoietin; type tumor necrosis factor alpha inhibitor;	
KW	TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNF;	
KW	the alpha peptide; pro-mimetic peptide; EMP; VEGF antagonist;	
KW	RNase inhibitor; antithrombotic; antitumor; immunosuppressive;	
KW	cytotoxic; antirheumatic; antifibrotic; antidiabetic; ophthalmological;	
KW	antianemic; anorectic; antifertility; haemostatic; dermatological;	
KW	neuroprotective; inflammatory; diuretic; autoimmune disease; linear growth;	
KW	cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;	
KW	sleep disorder; neurological degenerative disease; anaemia;	
KW	thrombocytopenia; metastatic tumour; systemic lupus erythematosus;	
KW	Panconi's syndrome.	
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FN	WO200193525-A2.	

PR 08 NOV 2001.  
 XX  
 PF 02 MAY 2002; 2001W; 0314430.  
 XX  
 PF 03 MAY 2002; 2001GS; 0543260.  
 XX  
 PA (AMCEN) AMCEN INC.  
 PF Peptide BL, Liu C, Choeatham JR, Boone LV, Gudas JM.  
 XX WPI: 2002-166142/17.  
 XX  
 XX Novel vehicle peptide molecule or its multimers useful for treating  
 PF inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
 PF diabetic retinopathy, obesity, sleep disorders and infertility.  
 XX  
 PF Claim 9; Page 5; 17pp; English.  
 XX  
 XX The present invention describes a vehicle-peptide molecule (I) or its  
 XX multimers. (I) can have anti-inflammatory, anti-tumor, immunosuppressive,  
 XX cytostatic, antirheumatic, antifertility, antidiabetic, ophthalmological,  
 XX antineoplastic, anorectic, antifertility, haemostatic, dermatological and  
 XX neuro-protective activities. (I) can be used as a therapeutic or  
 XX prophylactic agent as well as for screening purposes. (I) is useful for  
 XX diagnosing diseases characterised by dysfunction of their associated  
 XX protein of interest, for identifying normal or abnormal proteins of  
 XX interest, as a part of diagnostic kit to detect the presence of their  
 XX proteins of interest in a biological sample. Additionally, (I) is useful  
 XX for treating inflammatory and autoimmune diseases, tumor growth, cancer,  
 XX rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
 XX infertility, and neurological degenerative diseases. (I), comprising  
 XX pharmacologic compounds are useful for treating disorders characterised by  
 XX low red blood cell levels such as anemia. The pharmacologic comprising  
 XX compounds are useful for treating conditions that involve an existing  
 XX medication or a related biological condition expected to have a negative  
 XX deficiency, such as thrombocytopenia, aplastic anemia, metastatic  
 XX tumor which result in thrombocytopenia, systemic lupus erythematosus,  
 XX and Fanconi's syndrome. AB672463 to AB674426 and AB676694 to AB677777  
 XX represent amino acid and nucleic acid sequences used in the  
 XX exemplification of the present invention.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 67.00%; Score 64; DB Z6; Length 18;  
 Best Local Similarity 100.00%; Ident. No. 0.0041;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 TGHAVRAIGRLSS 22  
 DE 11 TGHAVRAIGRLSS 18  
 RESULT 9  
 AMB0070  
 ID AMB0070 standard; Peptide: 23 AA.  
 XX  
 XX AMB0070;  
 XX  
 XX 06 SEP 2002 (first entry)  
 XX  
 XX Partial amino acid sequence of myosin light chain kinase protein.  
 XX  
 XX Biosensor protein: green fluorescent protein; GFP; calmodulin sensor;  
 XX fluorescent; myosin light chain kinase.  
 XX  
 XX Unpublished.  
 XX  
 PF EPI-209147 AL.  
 XX  
 XX 29 MAY 2002.  
 XX  
 XX 21 NOV 2001; 2001EP 0127770.  
 XX

PR 22 NOV 2001; 2001EP 0127770.  
 XX  
 PF (AKAZ) AKAZAKI KAI KIKI INSL.  
 XX  
 PF NAKAI J.  
 XX  
 DR WPI: 2002-464878/50.  
 XX  
 XX Producing a biosensor protein capable of regulating fluorescence  
 PF property of green fluorescent protein comprises predicting an amino acid  
 PF residue that affects fluorescence, and fusing with a functional  
 PF molecule.  
 XX  
 PS Claim 14(b); Page 49; 49pp; English.  
 XX  
 XX The invention relates to producing a biosensor protein capable of  
 XX regulating a fluorescence property of green fluorescent protein (GFP).  
 XX This comprises predicting an amino acid affecting a fluorescence property  
 XX of GFP, producing fusion proteins with GFP and functional molecule(s),  
 XX reacting with a factor affecting the conformation of the functional  
 XX molecules and screening a fusion protein exhibiting a change in the  
 XX fluorescence property. The method is useful for producing a biosensor  
 XX protein (especially a calmodulin-sensing biosensor protein) capable of  
 XX regulating a fluorescence property of GFP. The method of producing  
 XX proteins with a unique structure produces proteins with a high  
 XX sensitivity, unlike prior art methods producing proteins with low  
 XX sensitivity. A specific detection device is not needed. The current  
 XX sequence represents a partial amino acid sequence of Epsin light chain  
 XX kinase protein that is used in the construction of a biosensor of the  
 XX invention.  
 SQ Sequence 21 AA;  
 Query Match 65.00%; Score 60; DB Z6; Length 21;  
 Best Local Similarity 71.43%; Ident. No. 0.0147;  
 Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 SLKASLGLGHAIVRAIGRLSS 22  
 DE 11 SLKASLGLGHAIVRAIGRLSS 21  
 RESULT 10  
 AMB0451  
 ID AMB0451 standard; Protein: 1953 AA.  
 XX  
 XX AMB0451;  
 XX  
 XX 08 MAY 2002 (first entry)  
 XX  
 XX Protein MYLK differentially expressed in breast cancer tissue.  
 XX  
 XX Human; diagnosis of breast cancer; endometrial cancer; breast tumor;  
 XX MYLK; mitotic activity index; cytostatic.  
 XX  
 XX Homo Sapiens.  
 XX  
 PF W0200210436 A2.  
 XX  
 PF 07 FEB 2002.  
 XX  
 XX 27-JUL-2001; 2001W; 0529642.  
 XX  
 PF 28 JUL 2001; 2001GS; 2220934.  
 XX  
 XX (BCHM) BRICHAM & WOMENS HOSPITAL INC.  
 PF (BAAK/) BAAK J.  
 XX  
 PF BAAK J., Mutter GL.  
 XX  
 DR WPI: 2002-180084/23.  
 DR N PSDR; AMK 65571.  
 XX

PT Diagnosis of breast cancer comprises determining expression of nucleic  
 PT acid molecules or expression products that are differentially expressed  
 PT in normal and malignant tissue.

XX Claim 47: Page 190-201; 219pp; English.

XX The present invention relates to a method for diagnosing breast cancer  
 CC in a subject suspected of having endometrial cancer. The method  
 CC comprises determining the expression of a set of human genes or  
 CC expression products in an endometrial sample suspected of being  
 CC cancerous. The human genes of the invention are differentially  
 CC expressed in breast tumors characterized as high or low MAI (mitotic  
 CC activity index). These sets of genes can be used to discriminate between  
 CC high and low MAI breast tumors. The invention also provides RNA and  
 CC protein microarrays for analysing the expression of the human genes and  
 CC their protein products. The methods and arrays are useful for the  
 CC diagnosis and prognosis of endometrial cancer, selecting and monitoring  
 CC treatment regimens, and identification of compounds useful for the  
 CC treatment of endometrial cancer. AAB4431, AAB4436 represent the human  
 CC proteins of the invention that are differentially expressed in breast  
 CC cancer tissue.

XX Sequence 1953 AA:

Query Match 53.2%; Score 58; DB 23; Length 1953;

Best Local Similarity 73.7%; Pred. No. 3.5;

Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 PRAS1GIGHAVPALEPLSS 22

II II:|||||

DB 1781 RRRWRKTSNAVPALEPLSS 1740

RESULT 11

AAB41523

ID AAB41523 standard; Protein: 177 AA.

XX AAB41523;

XX 22-099-2002 (first entry)

DE Human ovarian antigen HVVA022, SEQ ID NO:2655

XX human ovarian antigen, entry: ovarian, breast, cancer, tumoral,  
 FW ovarian cancer; breast cancer; tumor; reproductive system disorder;  
 FW infertility; pregnancy disorder; amenorrhea; polycystic ovary syndrome;  
 FW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 FW inflammatory condition; immune disorder; blood disorder;  
 FW cardiovascular disorder; respiratory disorder; neurological disorder;  
 FW gastrointestinal disorder; urinary system disorder; drug screening;  
 FW gene therapy; chromosome mapping; forensic analysis;  
 FW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 FW anti-inflammation; synovial; reproductive; chondrosarcoma cell.

XX Homo sapiens.

OS

XX W0200200677 A1.

FW

XX 03-JAN-2002.

XX 07-JUN-2001; 2001W0-US18563.

XX 07-JUN-2000; 2000US-209467P.

FW (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI: 2002-147878/19.

DE N-PSUR; ABQ54600.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.

PT ovarian cancer), immune disorders, cardiovascular disorders and  
 PT neurological diseases.

XX Claim 11: SEQ ID NO 2655; 292pp; English.

XX The invention relates to 2176 novel human ovarian antigens (AAB41104-  
 CC AAB43499) and to cDNAs encoding them (AAB41101-AAB43405), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosis,  
 CC treating, preventing or preventing relapse of, and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumors of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, amenorrhea,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders, ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity, the polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention.  
 CC Note: the sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from Wipo  
 CC at [http://wipo.int/pub/published\\_pat\\_sequences](http://wipo.int/pub/published_pat_sequences).

XX Sequence 177 AA:

Query Match 52.4%; Score 57; DB 23; Length 177;

Best Local Similarity 64.6%; Pred. No. 0.4;

Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 TSTPBASTCTCHAVPALEPLSS 22

II II:|||||

DE 2 TSGALSERTESAVPALEPLSS 23

RESULT 12

AAB56489

ID AAB56489 standard; Protein: 181 AA.

XX AAB56489;

XX 10-MAY-2001 (first entry)

XX

DE Human prostate cancer antigen protein sequence SEQ ID NO:967.

XX

XX Human, prostate cancer, prostate cancer antigen, detection; diagnosis;

FW neuroprotective; cytostatic; cardiac; immunomodulatory; muscular;

FW cellular; gastrointestinal; nephrotic; antifibrotic; synovial;

FW antibacterial; gene therapy; neural, immune, reproductive; renal;

FW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;

FW wound; infectious disease.

XX

OS Homo sapiens.

XX W0200055174 A1.

FW

XX 21-SEP-2000.

XX 08-MAR-2000; 2000W0-US05988.

XX 12-MAY-1999; 99US-0124270.

XX



02 treatment of *L. pneumophila* infection by designing inhibitors of rtxA and  
 03 emf and the use of rtxA/emf proteins as vaccines. The method of  
 04 the invention is useful for isolating and identifying bacteria genes that  
 05 relate to virulence determinant (e.g. in species responsible for  
 06 bacteremia, diarrhoea, pneumonia, legionnaires' disease, meningitis,  
 07 urinary tract infection, pyelonephritis, cystitis and urethritis).  
 08 The gene sequences are useful as primers for detecting *L. pneumophila* and  
 09 hence diagnosing legionnaires' disease in a subject. The genes are useful  
 10 for preventing *L. pneumophila* infection in a subject by cloning them in  
 11 an organism, allowing the organism to express the gene, or cloning them  
 12 into a eukaryotic expression plasmid, and vaccinating the subject with  
 13 the organism or plasmid. The present sequence is the *L. pneumophila*  
 14 emf protein conserved carboxy terminal region.

XX Sequence 144 AA;

Query Match 47.7%; Score 52; DB 23; Length 144;  
 Best Local Similarity 55.0%; Pred. No. 1.9;  
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 KASNGTGHAVRAIGRLSST 23  
 : ||| ||| ||| ||| |||  
 DE 64 KAASLGNNGNAYAGLLSEI 103

# RESULT 15

AB062810  
 ID AB062810 standard; Protein; 913 AA.

XX A\*

XX AB062810;

XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SP2 ID NO 15222.

XX Drosophila: developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.

XX Drosophila melanogaster.

XX W0200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001W0-US09241.

XX 23-MAR-2000; 2000US-191647P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE ) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers FW;

XX WPI; 2001-656860/75.

XX N-PSDH; ARL06914.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 genes from Drosophila and for elucidating cell signalling and cell-cell  
 interactions.

XX Disclosure; SEQ ID NO 15222; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
 capable of detecting 1000 or more genes from Drosophila. The invention is  
 useful in developmental biology and in elucidating cell signalling and  
 cell-cell interactions in higher eukaryotes for the development of  
 insecticides, therapeutics and pharmaceutical drugs. The invention  
 discloses genomic DNA sequences (AB01840-AB01851), expressed DNA  
 sequences (AB01840-AB01851) and the encoded proteins  
 (AB057737-AB072072).

XX The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic format directly from WIPO  
 at [http://wipo.int/pub/published\\_pat\\_sequences](http://wipo.int/pub/published_pat_sequences).

XX Sequence 913 AA;

Query Match 45.0%; Score 49; DB 22; Length 913;  
 Best Local Similarity 45.0%; Pred. No. 40;  
 Matches 9; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 LPFASLCTGHANPAIGRLSS 22

DE 557 LPFKWKTGNATRAIGRMAN 576

Search completed: January 2, 2003, 12:28:06  
 Job time : 33 secs



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M protein: protein search, using sw model

Run on: January 2, 2003, 12:26:41; Search time: 12 seconds (without alignments)

Filter: US 09 786 317 2

Perfect Score: 100

Sequence: 1 ISLRRASTAGHVAVALGRSS1 24

Scoring table: K=0.0962

Gapop 11.0, Gapex 0.5

Sequences: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum db seq length: 9

Maximum db seq length: 20000000

Post processing: Maximum Match: 50

Maximum Match: 50

Listed first 45 summaries

Database:	Issued Patents AA*
1	US 09 786 317 2
2	US 09 786 317 2
3	US 09 786 317 2
4	US 09 786 317 2
5	US 09 786 317 2
6	US 09 786 317 2
7	US 09 786 317 2
8	US 09 786 317 2
9	US 09 786 317 2
10	US 09 786 317 2

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length 3B	10	Description
1	76	69.7	26	4	US 08 842 322 1
2	68	62.4	20	2	US 08 842 322 6
3	66	60.6	22	2	US 08 842 322 10
4	65	59.6	20	2	US 08 842 322 14
5	65	59.6	20	2	US 08 842 322 18
6	65	59.6	20	2	US 08 842 322 22
7	65	59.6	20	2	US 08 842 322 26
8	65	59.6	20	2	US 08 842 322 30
9	68	64.2	20	2	US 08 842 322 34
10	48	44.0	45	4	US 08 722 015A 147
11	47	44.1	45	4	US 08 722 015A 148
12	47	44.1	45	4	US 08 722 015A 149
13	47	44.1	45	4	US 08 722 015A 150
14	44	40.4	45	4	US 08 722 015A 151
15	42	38.1	45	4	US 08 722 015A 152
16	41	37.6	45	4	US 08 722 015A 153
17	41	37.6	45	4	US 08 722 015A 154
18	40	36.7	45	4	US 08 722 015A 155
19	40	36.7	45	4	US 08 722 015A 156
20	39.5	36.2	1279	1	US 09 724 096 2
21	39.5	36.2	1279	1	US 09 724 096 3
22	39.5	36.2	1279	1	US 09 724 096 4
23	39	35.8	133	2	US 08 820 825 12
24	39	35.8	133	2	US 08 820 825 13
25	39	35.8	133	2	US 08 820 825 14
26	39	35.8	133	2	US 08 820 825 15
27	39	35.8	133	2	US 08 820 825 16

28	39	35.8	133	2	US 08 820 825 17
29	39	35.8	133	2	US 08 820 825 18
30	39	35.8	133	2	US 08 820 825 19
31	39	35.8	133	2	US 08 820 825 20
32	39	35.8	133	2	US 08 820 825 21
33	39	35.8	133	2	US 08 820 825 22
34	39	35.8	133	2	US 08 820 825 23
35	39	35.8	133	2	US 08 820 825 24
36	39	35.8	133	2	US 08 820 825 25
37	39	35.8	133	2	US 08 820 825 26
38	39	35.8	133	2	US 08 820 825 27
39	39	35.8	133	2	US 08 820 825 28
40	39	35.8	133	2	US 08 820 825 29
41	39	35.8	133	2	US 08 820 825 30
42	39	35.8	133	2	US 08 820 825 31
43	39	35.8	133	2	US 08 820 825 32
44	39	35.8	133	2	US 08 820 825 33
45	39	35.8	133	2	US 08 820 825 34

ALIGNMENTS

RESULT 1  
US-08 842 322 1  
Sequence 1, Application US/08042422  
Patent No. 6,476,257  
GENERAL INFORMATION:  
APPLICANT: Persechini, Anthony  
TITLE OF INVENTION: METHOD BY FEEL CHAMBERS OF LIBARO  
FIELD OF INVENTION: METHOD BY FEEL CHAMBERS OF LIBARO  
NUMBER OF SEQUENCES: 34  
COMPUTER SOFTWARE ADDRESS:  
ADDRESS: 1111 R. HANCOCK, LINDA, N. J. 07036  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14604  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: Patent In Release #1.0, Version #1.00  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/842 322  
FILING DATE:  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: BRAMAN, SUSAN J.  
REGISTRATION NUMBER: 44,103  
LEFT HAND SIDE: 1111 R. HANCOCK, LINDA, N. J. 07036  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1646  
TELEFAX: 716-263-1600  
INFORMATION IN DB: 100  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US 08 842 322-1

Query Match:	69.7%	Score: 76	DB 4	Length: 26
Best Local Similarity:	76.4%	Prod. No. 6,476,257		
Matches:	197	Conserved:	67	Mismatches: 6
QY	1	ISLRRASTAGHVAVALGRSS1 24		
	1	1111111111111111		
DB	2	ISLRRASTAGHVAVALGRSS1 24		

```

RESULT 4
US-08-542-927-5
: Sequence 6, Application US/08542927
: Patent No. 5998580
: GENERAL INFORMATION:
: APPLICANT: Fay, Fredric
: APPLICANT: Carraway, Robert
: APPLICANT: Ikebe, Mitsuo
: APPLICANT: Walker, Jeffrey
: TITLE OF INVENTION: PHOTOLABILE CAGED MACROMOLECULES
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2904
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 08/08542927
: FILING DATE: 13-OCT-1995
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Feltz
: REGISTRATION NUMBER: 40,162
: REFERENCE/DECKET NUMBER: 04020,045901
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5970
: TELEFAX: 617/542-9906
: TELETYPE: 200154
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 20 amino acids
: TYPE: amino acid
: TOPOLOGY: not relevant
: MOLECULE TYPE: protein
: FEATURE:
: OTHER INFORMATION: Xaa at position 5 contains a caged tyrosine.
US-08-542-927-5
Query Match 62.4% Score 68; DB 2; Length 20;
Best Local Similarity 78.9%; Pred. No. 0.0003;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 PRASADCHAVRAIGRESS 22
II IIIIIIIIIII
DB 2 PRASADCHAVRAIGRESS 20
II IIIIIIIIIII

RESULT 5
5182262-10
: Patent No. 5182262
: APPLICANT: LEBO, THOMAS
: TITLE OF INVENTION: CALMODULIN BINDING PEPTIDE DERIVATIVES
: NUMBER OF SEQUENCES: 15
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 08/02718,172
: FILING DATE: 02-MAR-1989
: SEQ ID NO:10:
: LENGTH: 22
5182262-10
Query Match 60.6% Score 66; DB 6; Length 22;
Best Local Similarity 75.0%; Pred. No. 0.00023;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 4 PRASADCHAVRAIGRESS 24
II IIIIIIIIIII
DB 3 PRASADCHAVRAIGRESS 22
II IIIIIIIIIII

RESULT 4
US-08-818-253-10
: Sequence 10, Application US/08818253
: Patent No. 5995204
: GENERAL INFORMATION:
: APPLICANT: Tsien, Roger Y.
: APPLICANT: Miyawaki, Atsushi
: TITLE OF INVENTION: FLUORESCENT PROTEIN SUBSTRATES FOR
: TITLE OF INVENTION: DETECTION OF ANALYTES
: NUMBER OF SEQUENCES: 61
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 425 Executive Square, Suite 1400
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: FASTSEQ for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 08/08818253
: FILING DATE: 14-MAR-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Hallie, Ph.D., Lisa A.
: REGISTRATION NUMBER: 48,347
: REFERENCE/DECKET NUMBER: 07257/043001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/678-5070
: TELEFAX: 619/678-5099
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 20 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: polypeptide
US-08-818-253-10
Query Match 59.4% Score 65; DB 2; Length 20;
Best Local Similarity 78.9%; Pred. No. 0.0003;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 PRASADCHAVRAIGRESS 22
II IIIIIIIIIII
DB 2 PRASADCHAVRAIGRESS 20
II IIIIIIIIIII

RESULT 5
US-08-542-927-5
: Sequence 5, Application US/08542927
: Patent No. 5998580
: GENERAL INFORMATION:
: APPLICANT: Fay, Fredric
: APPLICANT: Carraway, Robert
: APPLICANT: Ikebe, Mitsuo
: APPLICANT: Walker, Jeffrey
: TITLE OF INVENTION: PHOTOLABILE CAGED MACROMOLECULES
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA

```

1 COUNTRY: USA  
 2 ZIP: 14603  
 3 COMPUTER READABLE FORM:  
 4 MEDIUM TYPE: Floppy disk  
 5 COMPUTER: IBM PC compatible  
 6 OPERATING SYSTEM: PC DOS/MS DOS  
 7 SOFTWARE: Patent In Release #1.0, Version #1.0  
 8 CURRENT APPLICATION DATA:  
 9 APPLICATION NUMBER: US/09/42,927  
 10 FILING DATE: 13 Oct 1995  
 11 CLASSIFICATION: 5.0  
 12 ATTORNEY/AGENT INFORMATION:  
 13 NAME: Clark, Paul L.  
 14 REGISTRATION NUMBER: 40,162  
 15 REFERENCE TO PUBLICATION:  
 16 TELECOMMUNICATION INFORMATION:  
 17 TELEPHONE: 617/642 5076  
 18 TELEFAX: 617/642 8066  
 19 FILING DATE: 200154  
 20 INFORMATION FOR SEQ ID NO: 5:  
 21 SEQUENCE CHARACTERISTICS:  
 22 LENGTH: 20 amino acids  
 23 TYPE: amino acid  
 24 STRANDNESS: not relevant  
 25 TOPOLOGY: both  
 26 MOLECULE TYPE: protein  
 27 US 09-786-317-2

Query Match 59.6% Score 65; DB 4; Length 20;  
 Best Local Similarity 76.9% Prod. No. 0.0004  
 Matches 15; Conserved 0; Mismatches 4; Indels 0; Gaps 0;

27 4 REASJGTHAVAVAGRLSS 22

db 2 RRRWJKTHAVAVAGRLSS 20

RESULT 7  
 US 09-816-919-26  
 1 Sequence 26; Application US/09/46919  
 2 Patent No. 6469154  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Tsien, Roger Y.  
 5 TITLE OF INVENTION: EPITOPES FROM SEV-1  
 6 TITLE OF INVENTION: EPITOPES FROM SEV-1  
 7 FILE REFERENCE: 02/57/04201  
 8 CURRENT APPLICATION NUMBER: US/09/46919  
 9 NUMBER OF SEQ ID NOS: 5  
 10 SOFTWARE: FASTSEQ for Windows Version 4.0  
 11 SEQ ID NO: 1  
 12 LENGTH: 20  
 13 TYPE: PRT  
 14 ORGANISM: Medcarris gallopato  
 15 US 09-816-919-26

Query Match 59.6% Score 65; DB 4; Length 20;  
 Best Local Similarity 76.9% Prod. No. 0.0004  
 Matches 15; Conserved 0; Mismatches 4; Indels 0; Gaps 0;

27 4 REASJGTHAVAVAGRLSS 22

db 2 RRRWJKTHAVAVAGRLSS 20

RESULT 7  
 US 09-816-919-26  
 1 Sequence 26; Application US/09/46919  
 2 Patent No. 6469154  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Tsien, Roger Y.  
 5 TITLE OF INVENTION: EPITOPES FROM SEV-1  
 6 TITLE OF INVENTION: EPITOPES FROM SEV-1  
 7 FILE REFERENCE: 02/57/04201  
 8 CURRENT APPLICATION NUMBER: US/09/46919  
 9 NUMBER OF SEQ ID NOS: 5  
 10 SOFTWARE: FASTSEQ for Windows Version 4.0  
 11 SEQ ID NO: 1  
 12 LENGTH: 20  
 13 TYPE: PRT  
 14 ORGANISM: Medcarris gallopato  
 15 US 09-816-919-26

1 TITLE OF INVENTION: PATENT BY SEV-1  
 2 NUMBER OF SEQUENCES: 5  
 3 CORRESPONDENCE ADDRESS:  
 4 ADDRESSEE: NIXON, BARBARA, EVANS & LEWIS LLP  
 5 STREET: Clinton Square, P.O. Box 100  
 6 CITY: Rochester  
 7 STATE: New York  
 8 COUNTRY: USA  
 9 ZIP: 14603  
 10 COMPUTER READABLE FORM:  
 11 MEDIUM TYPE: Floppy disk  
 12 COMPUTER: IBM PC compatible  
 13 OPERATING SYSTEM: PC DOS/MS DOS  
 14 SOFTWARE: Patent In Release #1.0, Version #1.0  
 15 CURRENT APPLICATION DATA:  
 16 APPLICATION NUMBER: US/09/42,927  
 17 FILING DATE:  
 18 CLASSIFICATION: 4.0  
 19 ATTORNEY/AGENT INFORMATION:  
 20 NAME: BRAMAN, SUSAN J.  
 21 REGISTRATION NUMBER: 44,104  
 22 REFERENCE TO PUBLICATION:  
 23 TELECOMMUNICATION INFORMATION:  
 24 TELEPHONE: 716-263-1646  
 25 TELEFAX: 716-263-1640  
 26 INFORMATION FOR SEQ ID NO: 4:  
 27 SEQUENCE CHARACTERISTICS:  
 28 LENGTH: 20 amino acids  
 29 TYPE: amino acid  
 30 STRANDNESS: not relevant  
 31 TOPOLOGY: linear  
 32 MOLECULE TYPE: peptide  
 33 US 09-816-919-26

Query Match 59.6% Score 65; DB 4; Length 20;  
 Best Local Similarity 76.9% Prod. No. 0.0004  
 Matches 15; Conserved 0; Mismatches 4; Indels 0; Gaps 0;

27 4 REASJGTHAVAVAGRLSS 22

db 2 RRRWJKTHAVAVAGRLSS 20

RESULT 8  
 US 09-816-919-26  
 1 Sequence 26; Application US/09/46919  
 2 Patent No. 6469154  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Tsien, Roger Y.  
 5 TITLE OF INVENTION: EPITOPES FROM SEV-1  
 6 TITLE OF INVENTION: EPITOPES FROM SEV-1  
 7 FILE REFERENCE: 02/57/04201  
 8 CURRENT APPLICATION NUMBER: US/09/46919  
 9 NUMBER OF SEQ ID NOS: 5  
 10 SOFTWARE: FASTSEQ for Windows Version 4.0  
 11 SEQ ID NO: 26  
 12 LENGTH: 20  
 13 TYPE: PRT  
 14 ORGANISM: Medcarris gallopato  
 15 US 09-816-919-26

Query Match 59.6% Score 65; DB 4; Length 20;  
 Best Local Similarity 76.9% Prod. No. 0.0004  
 Matches 15; Conserved 0; Mismatches 4; Indels 0; Gaps 0;

27 4 REASJGTHAVAVAGRLSS 22

db 2 RRRWJKTHAVAVAGRLSS 20

RESULT 9  
 US 09-816-919-26

Query Match 53.2% Score 58, DB 2, Length 20;

Best Local Similarity 73.7% Pred No. 0.004;

Matches 14: Conservative 0, Mismatches 5, Indels 0;

Q7 4 PRASLCTGHAVPAICPL 20

Db 2 PRFWKTXHAVPAICPLSS 20

RESULT 10

US-08-722-015A-147

; Sequence 147, Application US/08722015A

; Patent No. 6379881

; GENERAL INFORMATION:

; APPLICANT: Fouchier, Ronaldus A.M.

; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCR

; FILE REFERENCE: 9250.25

; CURRENT FILING DATE: 1996-11-19

; NUMBER OF SEQ ID NOS: 258

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 147

; LENGTH: 35

; TYPE: PR

; ORGANISM: Human Immunodeficiency Virus Isolate H72-8.S

US-08-722-015A-147

; Sequence 147, Application US/08722015A

; Patent No. 6379881

; GENERAL INFORMATION:

; APPLICANT: Fouchier, Ronaldus A.M.

; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCR

; FILE REFERENCE: 9250.25

; CURRENT FILING DATE: 1996-11-19

; NUMBER OF SEQ ID NOS: 258

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 147

; LENGTH: 35

; TYPE: PR

; ORGANISM: Human Immunodeficiency Virus Isolate H72-8.S

US-08-722-015A-147

; Sequence 147, Application US/08722015A

; Patent No. 6379881

; GENERAL INFORMATION:

; APPLICANT: Fouchier, Ronaldus A.M.

; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCR

; FILE REFERENCE: 9250.25

; CURRENT FILING DATE: 1996-11-19

; NUMBER OF SEQ ID NOS: 258

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 147

; LENGTH: 35

; TYPE: PR

; ORGANISM: Human Immunodeficiency Virus Isolate H72-8.S

US-08-722-015A-147

; Sequence 147, Application US/08722015A

; Patent No. 6379881

; GENERAL INFORMATION:

; APPLICANT: Fouchier, Ronaldus A.M.

; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCR

; FILE REFERENCE: 9250.25

; CURRENT FILING DATE: 1996-11-19

; NUMBER OF SEQ ID NOS: 258

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 147

; LENGTH: 35

; TYPE: PR

; ORGANISM: Human Immunodeficiency Virus Isolate H72-8.S

US-08-722-015A-147

; Sequence 147, Application US/08722015A

; Patent No. 6379881

; GENERAL INFORMATION:

; APPLICANT: Fouchier, Ronaldus A.M.

; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCR

; FILE REFERENCE: 9250.25

; CURRENT FILING DATE: 1996-11-19

; NUMBER OF SEQ ID NOS: 258

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 147

; LENGTH: 35

; TYPE: PR

; ORGANISM: Human Immunodeficiency Virus Isolate H72-8.S

US-08-722-015A-147

; Sequence 147, Application US/08722015A

; Patent No. 6379881

; GENERAL INFORMATION:

; APPLICANT: Fouchier, Ronaldus A.M.

Query Match 53.2% Score 58, DB 2, Length 20;

Best Local Similarity 73.7% Pred No. 0.004;

Matches 14: Conservative 0, Mismatches 5, Indels 0;

Q7 4 PRASLCTGHAVPAICPL 20

Db 2 PRFWKTXHAVPAICPLSS 20

RESULT 10

US-08-722-015A-147

; Sequence 147, Application US/08722015A

; Patent No. 6379881

; GENERAL INFORMATION:

; APPLICANT: Fouchier, Ronaldus A.M.

; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCR

; FILE REFERENCE: 9250.25

; CURRENT FILING DATE: 1996-11-19

; NUMBER OF SEQ ID NOS: 258

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 147

; LENGTH: 35

; TYPE: PR

; ORGANISM: Human Immunodeficiency Virus Isolate H72-8.S

US-08-722-015A-147

; Sequence 147, Application US/08722015A

; Patent No. 6379881

; GENERAL INFORMATION:

; APPLICANT: Fouchier, Ronaldus A.M.

; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCR

; FILE REFERENCE: 9250.25

; CURRENT FILING DATE: 1996-11-19

; NUMBER OF SEQ ID NOS: 258

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 147

; LENGTH: 35

; TYPE: PR

; ORGANISM: Human Immunodeficiency Virus Isolate H72-8.S

US-08-722-015A-147

; Sequence 147, Application US/08722015A

; Patent No. 6379881

; GENERAL INFORMATION:

; APPLICANT: Fouchier, Ronaldus A.M.

; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCR

; FILE REFERENCE: 9250.25

; CURRENT FILING DATE: 1996-11-19

; NUMBER OF SEQ ID NOS: 258

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 147

; LENGTH: 35

; TYPE: PR

; ORGANISM: Human Immunodeficiency Virus Isolate H72-8.S

US-08-722-015A-147

; Sequence 147, Application US/08722015A

; Patent No. 6379881

; GENERAL INFORMATION:

; APPLICANT: Fouchier, Ronaldus A.M.

; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCR

; FILE REFERENCE: 9250.25

; CURRENT FILING DATE: 1996-11-19

; NUMBER OF SEQ ID NOS: 258

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 147

; LENGTH: 35

; TYPE: PR

; ORGANISM: Human Immunodeficiency Virus Isolate H72-8.S

US-08-722-015A-147

; Sequence 147, Application US/08722015A

; Patent No. 6379881

; GENERAL INFORMATION:

; APPLICANT: Fouchier, Ronaldus A.M.

; TITLE OF INVENTION: NUCLEIC ACIDS AND METHODS FOR THE DISCRIMINATION BETWEEN SYNCR

; FILE REFERENCE: 9250.25

; CURRENT FILING DATE: 1996-11-19

; NUMBER OF SEQ ID NOS: 258

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 147

; LENGTH: 35

; TYPE: PR

; ORGANISM: Human Immunodeficiency Virus Isolate H72-8.S

US-08-722-015A-147

; Sequence 147, Application US/08722015A

; Patent No. 6379881

; GENERAL INFORMATION:

; APPLICANT: Fouchier, Ronaldus A.M.

APPLICANT: Schottmeyer, Johanna  
 TITLE OF INVENTION: REVERSE AIDS AND MECHANISMS FOR THE DIFFERENTIATION BETWEEN SYNCRITIC  
 TITLE OF INVENTION: REVERSE AIDS AND MECHANISMS FOR THE DIFFERENTIATION BETWEEN SYNCRITIC  
 FILE REFERENCE: 9250.25  
 CURRENT APPLICATION NUMBER: 03/08/722.015A  
 CURRENT FILING DATE: 1996.11.19  
 NUMBER OF SEQ ID NOS: 258  
 SOFTWARE: Patent in version 4.1  
 SEQ ID NO 149  
 LENGTH: 45  
 TYPE: PPT  
 ORGANISM: Human Immunodeficiency Virus Isolate H72.8  
 US 09 722 015A 149

Query Match 43.1%; Score 47; DB 4; Length 45;  
 Best Local Similarity 42.9%; Prod. No. 0.44;  
 Matches 5; Conservation 5; Mismatches 5; Indels 5; Gaps 0;

27 4 PRASADCHAVAKHAR 20  
 11 11 11 11 11 11  
 14 10 PRISHPAKHAR 20

RESULT 14  
 US 09 722 015A 148  
 Applicant: Schottmeyer, Johanna  
 Patent No. 6379861  
 GENERAL INFORMATION:  
 APPLICANT: Schottmeyer, Johanna A.M.  
 TITLE OF INVENTION: REVERSE AIDS AND MECHANISMS FOR THE DIFFERENTIATION BETWEEN SYNCRITIC  
 TITLE OF INVENTION: REVERSE AIDS AND MECHANISMS FOR THE DIFFERENTIATION BETWEEN SYNCRITIC  
 FILE REFERENCE: 9250.25  
 CURRENT APPLICATION NUMBER: 03/08/722.015A  
 CURRENT FILING DATE: 1996.11.19  
 NUMBER OF SEQ ID NOS: 258  
 SOFTWARE: Patent in version 4.1  
 SEQ ID NO 148  
 LENGTH: 45  
 TYPE: PPT  
 ORGANISM: Human Immunodeficiency Virus Isolate H72.8  
 US 09 722 015A 148

Query Match 40.4%; Score 44; DB 4; Length 45;  
 Best Local Similarity 47.1%; Prod. No. 1.33  
 Matches 4; Conservation 4; Mismatches 5; Indels 5; Gaps 0;

27 4 PRASADCHAVAKHAR 20  
 11 11 11 11 11 11  
 14 10 PRISHPAKHAR 20

RESULT 15  
 US 09 722 015A 144  
 Applicant: Schottmeyer, Johanna  
 Patent No. 6379861  
 GENERAL INFORMATION:  
 APPLICANT: Schottmeyer, Johanna A.M.  
 TITLE OF INVENTION: REVERSE AIDS AND MECHANISMS FOR THE DIFFERENTIATION BETWEEN SYNCRITIC  
 TITLE OF INVENTION: REVERSE AIDS AND MECHANISMS FOR THE DIFFERENTIATION BETWEEN SYNCRITIC  
 FILE REFERENCE: 9250.25  
 CURRENT APPLICATION NUMBER: 03/08/722.015A  
 CURRENT FILING DATE: 1996.11.19  
 NUMBER OF SEQ ID NOS: 258  
 SOFTWARE: Patent in version 4.1  
 SEQ ID NO 144  
 LENGTH: 45  
 TYPE: PPT  
 ORGANISM: Human Immunodeficiency Virus Isolate H72.25.8  
 US 09 722 015A 144

Query Match 40.5%; Score 42; DB 4; Length 45;

Best Local Similarity 47.1%; Prod. No. 2.63  
 Matches 8; Conservation 5; Mismatches 5; Indels 5; Gaps 0;  
 27 4 PRASADCHAVAKHAR 20  
 11 11 11 11 11 11  
 14 10 PRISHPAKHAR 20

Search completed: January 2, 2003, 12:29:47  
 Job time : 14 secs

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? CURRENT FILING DATE: 2000-04-20  
 ? PRIOR APPLICATION NUMBER: 08/018,252  
 ? FILING DATE: 1997-03-14  
 ? NUMBER OF SEQ ID NOS: 56  
 ? SOFTWARE: FastSeq for Windows Version 4.0  
 ? SEQ ID NO 10  
 ? LENGTH: 20  
 ? TYPE: PRT  
 ? ORGANISM: *Mycobacterium tuberculosis*  
 US-09-554-000-10

Query Match: 59.5%; Score 65; DB 9; Length 20;  
 Best Local Similarity: 79.9%; Pred. No. 0.00021  
 Matches: 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0.

QY 4 PRASLCTGHAVRAIGRLSS 22  
 II IIIIIIIIIII  
 DB 2 RFWLKTGHAVRAIGRLSS 20

## RESULT 4

US-09-925-309-957  
 ? Sequence 957, Application US/09425300  
 ? Patent No. US20020151681A1  
 ? GENERAL INFORMATION:

? APPLICANT: Craig Rosen,  
 ? APPLICANT: Steve Rubin  
 ? TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ? FILE REFERENCE: P0101  
 ? CURRENT APPLICATION NUMBER: US/09/925,300  
 ? CURRENT FILING DATE: 2001-08-10  
 ? PRIOR APPLICATION NUMBER: PCT/US00/05988  
 ? PRIOR FILING DATE: 2000-03-08  
 ? PRIOR APPLICATION NUMBER: 60/224,270  
 ? PRIOR FILING DATE: 1999-03-12  
 ? NUMBER OF SEQ ID NOS: 1890  
 ? SOFTWARE: Patent In Ver. 2.0  
 ? SEQ ID NO 957  
 ? LENGTH: 181  
 ? TYPE: PRT  
 ? ORGANISM: *Homo sapiens*  
 ? FEATURE:  
 ? NAME/KEY: SITE  
 ? LOCATION: (163)  
 ? OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids  
 ? NAME/KEY: SITE  
 ? LOCATION: (175)  
 ? OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids  
 US-09-925-309-957

Query Match: 51.4%; Score 56; DB 10; Length 181;  
 Best Local Similarity: 92.8%; Pred. No. 0.0001  
 Matches: 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 10 TGHAVRAIGRLSS 22  
 II IIIIIIIIIII  
 DB 68 TGNVRAIGRLSS 80

## RESULT 4

US-09-815-242-11948  
 ? Sequence 11948, Application US/09815242  
 ? Patent No. US20020061569A1  
 ? GENERAL INFORMATION:

? APPLICANT: Haselbeck, Robert  
 ? APPLICANT: Ohlson, Karl L.  
 ? APPLICANT: Zyskind, Judith W.  
 ? APPLICANT: Wall, Daniel  
 ? APPLICANT: Trawick, John D.  
 ? APPLICANT: Carr, Grant J.  
 ? APPLICANT: Yamamoto, Robert T.  
 ? APPLICANT: Xu, H. Howard  
 ? TITLE OF INVENTION: Identification of Essential Genes in

? TITLE OF INVENTION: Prokaryotes  
 ? FILE REFERENCE: ELITRA.011A  
 ? CURRENT APPLICATION NUMBER: 09/09815242  
 ? CURRENT FILING DATE: 2001-03-21  
 ? PRIOR APPLICATION NUMBER: 60/191,078  
 ? PRIOR FILING DATE: 2000-03-21  
 ? PRIOR APPLICATION NUMBER: 60/206,848  
 ? PRIOR FILING DATE: 2000-05-23  
 ? PRIOR APPLICATION NUMBER: 60/207,727  
 ? PRIOR FILING DATE: 2000-05-26  
 ? PRIOR APPLICATION NUMBER: 60/242,578  
 ? PRIOR FILING DATE: 2000-10-23  
 ? PRIOR APPLICATION NUMBER: 60/253,625  
 ? PRIOR FILING DATE: 2000-11-27  
 ? PRIOR APPLICATION NUMBER: 60/257,931  
 ? PRIOR FILING DATE: 2000-12-22  
 ? PRIOR APPLICATION NUMBER: 60/269,308  
 ? PRIOR FILING DATE: 2001-02-16  
 ? NUMBER OF SEQ ID NOS: 14110  
 ? SOFTWARE: FastSeq for Windows Version 4.0  
 ? SEQ ID NO 11948  
 ? LENGTH: 457  
 ? TYPE: PRT  
 ? ORGANISM: *Pseudomonas aeruginosa*  
 US-09-815-242-11948

Query Match: 41.3%; Score 45; DB 10; Length 457;  
 Best Local Similarity: 52.9%; Pred. No. 9.9;  
 Matches: 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0.

QY 4 KRASLCTGHAVRAIGRL 20  
 II IIIII II IIIII  
 DB 403 PRALSGTGVQVQVGR 419

## RESULT 5

US-09-815-242-11922  
 ? Sequence 11922, Application US/09815242  
 ? Patent No. US20020061569A1  
 ? GENERAL INFORMATION:

? APPLICANT: Haselbeck, Robert  
 ? APPLICANT: Ohlson, Karl L.  
 ? APPLICANT: Zyskind, Judith W.  
 ? APPLICANT: Wall, Daniel  
 ? APPLICANT: Trawick, John D.  
 ? APPLICANT: Carr, Grant J.  
 ? APPLICANT: Yamamoto, Robert T.  
 ? APPLICANT: Xu, H. Howard  
 ? TITLE OF INVENTION: Identification of Essential Genes in  
 ? TITLE OF INVENTION: Prokaryotes  
 ? FILE REFERENCE: ELITRA.011A  
 ? CURRENT APPLICATION NUMBER: 09/09815242  
 ? CURRENT FILING DATE: 2001-03-21  
 ? PRIOR APPLICATION NUMBER: 60/191,078  
 ? PRIOR FILING DATE: 2000-03-21  
 ? PRIOR APPLICATION NUMBER: 60/206,848  
 ? PRIOR FILING DATE: 2000-05-23  
 ? PRIOR APPLICATION NUMBER: 60/207,727  
 ? PRIOR FILING DATE: 2000-05-26  
 ? PRIOR APPLICATION NUMBER: 60/242,578  
 ? PRIOR FILING DATE: 2000-10-23  
 ? PRIOR APPLICATION NUMBER: 60/253,625  
 ? PRIOR FILING DATE: 2000-11-27  
 ? PRIOR APPLICATION NUMBER: 60/257,931  
 ? PRIOR FILING DATE: 2000-12-22  
 ? PRIOR APPLICATION NUMBER: 60/269,308  
 ? PRIOR FILING DATE: 2001-02-16  
 ? NUMBER OF SEQ ID NOS: 14110  
 ? SOFTWARE: FastSeq for Windows Version 4.0  
 ? SEQ ID NO 11922  
 ? LENGTH: 477  
 ? TYPE: PRT  
 ? ORGANISM: *Pseudomonas aeruginosa*



US-09-815-242-11942

Query Match: 47.66% Score 41: DB 10: Length 477;

Best Local Similarity: 47.66% Prod. No. 41;

Matches 11: Conservative 0: Mismatches 6: Indels 0: Gaps 1:

QY 1 USRASHDIGHAV 19  
DB 70 L4QAEQDIGHAV 92

RESULT 6

US-09-815-242-11942

Sequence 44: Application US/0907050

Patent No. US20020091569A1

GENERAL INFORMATION:

APPLICANT: Baselbeck, Robert

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Yamamoto, Robert I.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA-011A

CURRENT APPLICATION NUMBER: 09/0915242

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 44

LENGTH: 91

TYPE: PRT

ORGANISM: Homo sapiens

FEATURES:

NAME/KEY: VARIANT

LOCATION: (46)

OTHER INFORMATION: when in Xaa may be any one of Ile or Met

US-09-815-242-11942

Query Match:

Best Local Similarity: 47.66% Score 41: DB 10: Length 81;

Matches 10: Conservative 0: Mismatches 5: Indels 0: Gaps 0:

QY 1 USRASHDIGHAV 19

DB 29 USRASHDIGHAV 44

RESULT 7

US-09-815-242-11942

Sequence 10947: Application US/0907050

Patent No. US20020091569A1

GENERAL INFORMATION:

APPLICANT: Baselbeck, Robert

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Yamamoto, Robert I.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA-011A

CURRENT APPLICATION NUMBER: 09/0915242

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 44

LENGTH: 91

TYPE: PRT

ORGANISM: Homo sapiens

FEATURES:

NAME/KEY: VARIANT

LOCATION: (46)

OTHER INFORMATION: when in Xaa may be any one of Ile or Met

US-09-815-242-11942

PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-03-21  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10947  
LENGTH: 461  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-815-242-11942

Query Match:

Best Local Similarity: 47.66% Score 41: DB 10: Length 461;

Matches 8: Conservative 0: Mismatches 5: Indels 0: Gaps 0:

QY 2 USRASHDIGHAV 14

DB 74 USRASHDIGHAV 86

RESULT 8

US-09-815-242-12112

Sequence 12112: Application US/0907050

Patent No. US20020091569A1

GENERAL INFORMATION:

APPLICANT: Baselbeck, Robert

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Yamamoto, Robert I.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA-011A

CURRENT APPLICATION NUMBER: 09/0915242

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12112

LENGTH: 454

TYPE: PRT

ORGANISM: Homo sapiens

FEATURES:

NAME/KEY: VARIANT

LOCATION: (46)

OTHER INFORMATION: when in Xaa may be any one of Ile or Met

US-09-815-242-12112

Query Match:

Best Local Similarity: 47.66% Score 41: DB 10: Length 454;

Matches 11: Conservative 0: Mismatches 5: Indels 1: Gaps 1:

QY 3 USRASHDIGHAV 22

DB 72 USRASHDIGHAV 92

```

RESULT 9
US-09-748-626-4263
; Sequence 4263, Application US/09748626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOHI, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09-748-626
; PRIOR APPLICATION NUMBER: JP 99/477484
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4263
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-748-626-4263

Query Match 37.2%; Score 40.5; DB 9; Length 575;
Best Local Similarity 64.3%; Pred. No. 66;
Matches 9; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 11 GHA-VRAIGRLSST 24
II IIIIIIIII
DB 525 GHVIRALGVSGT 538

RESULT 10
US-09-764-864-947
; Sequence 947, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P123
; CURRENT APPLICATION NUMBER: US/09-764-864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed (consult FALM or file wrapper)
; NUMBER OF SEQ ID NOS: 1793
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 947
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-947

Query Match 36.7%; Score 40; DB 10; Length 212;
Best Local Similarity 64.3%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 LUTGHAVRAIGRLS 21
II IIIIIIIII
DB 132 LGAGSVRAAGRAS 145

RESULT 11
US-09-738-626-4486
; Sequence 4486, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOHI, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09-738-626
; PRIOR APPLICATION NUMBER: JP 99/477484
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4486
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4486

Query Match 36.7%; Score 40; DB 9; Length 220;
Best Local Similarity 52.6%; Pred. No. 27;
Matches 10; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 7 SLATGHAVRAIG-RLSST 23
II IIIIIIIII
DB 140 ALGVDAHFRIGLRRLTAT 158

RESULT 12
US-09-737-149-25
; Sequence 25, Application US/09737149
; Patent No. US20020077466A1
; GENERAL INFORMATION:
; APPLICANT: Spaderna, Steven K
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Muralidhara, Padigattu
; APPLICANT: Spyrack, Kimberly A.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15046-620-GIP
; CURRENT APPLICATION NUMBER: US/09-737-149
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/170,564
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: 60/173,165
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: 60/173,362
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: 60/173,544
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/174,404
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 60/174,962
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 60/223,929
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 25
; LENGTH: 3034
; TYPE: PRT

```

1 ORGANISM: Mus musculus

US-09-786-317-2

Query Match  
Best Local Similarity 46.7% Score 47 DB 10 Length 4034  
Matches 9 Conserved 2 Mismatches 5 Indels 0 Gaps 0

QY 1 ESRRASLGHAVVA 16  
II III III III III

DB 2996 ESRRSSLSGSCVHA 2993

RESULT 14

US-09-786-317-2

Sequence 14.9% Application US/09737149

Patent No. US2002007466A1

GENERAL INFORMATION:

APPLICANT: Spadeford, Steven K

APPLICANT: Quinn, Kerry E.

APPLICANT: Shimko, Richard A.

APPLICANT: Muradkhani, Padiquan

APPLICANT: Stepek, Kimberly A.

TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same

FILE REFERENCE: 1566, 626, 617

CURRENT APPLICATION NUMBER: 60/174,165

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/174,164

PRIOR FILING DATE: 1999-12-13

PRIOR APPLICATION NUMBER: 60/174,165

PRIOR FILING DATE: 1999-12-27

PRIOR APPLICATION NUMBER: 60/174,162

PRIOR FILING DATE: 1999-12-27

PRIOR APPLICATION NUMBER: 60/174,164

PRIOR FILING DATE: 1999-12-27

PRIOR APPLICATION NUMBER: 60/174,164

PRIOR FILING DATE: 2000-01-04

PRIOR APPLICATION NUMBER: 60/174,162

PRIOR FILING DATE: 2000-01-07

PRIOR APPLICATION NUMBER: 60/224,929

PRIOR FILING DATE: 2000-08-09

NUMBER OF SEQ IDS NOS: 49

SOFTWARE: Patent In Vct. 2.0

SEQ ID No. 40

LENGTH: 4034

TYPE: PRI

ORGANISM: Mus musculus

US-09-786-317-2

Query Match  
Best Local Similarity 46.7% Score 47 DB 10 Length 4034  
Matches 9 Conserved 2 Mismatches 5 Indels 0 Gaps 0

QY 1 ESRRASLGHAVVA 16  
II III III III III

DB 2996 ESRRSSLSGSCVHA 2993

RESULT 14

US-09-786-317-2

Sequence 14.9% Application US/09737149

Patent No. US2002-05627A1

GENERAL INFORMATION:

APPLICANT: Bosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: P4102

CURRENT APPLICATION NUMBER: US/09737149

PRIOR FILING DATE: 2000-01-04

PRIOR APPLICATION NUMBER: P4102/09737149

PRIOR FILING DATE: 2000-01-07

PRIOR APPLICATION NUMBER: 60/174,164

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ IDS NOS: 1556

SOFTWARE: Patent In Vct. 2.0

SEQ ID No 1439

LENGTH: 78

TYPE: PRI

ORGANISM: Homo sapiens

FEATURES:

NAME/KEY: SITE

LOCATION: (71)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (72)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-786-317-2

Query Match

Best Local Similarity 46.2% Score 49 DB 10 Length 78

Matches 11 Conserved 27 Mismatches 6 Indels 4 Gaps 1

QY 4 PRASLGHAVVA VRALGSS 22

II III III III III

DB 47 RTRKATGRVAVNVGICRKSAS 68

RESULT 15

US-09-786-317-2

Sequence 14.9% Application US/09737149

Patent No. US2002007466A1

GENERAL INFORMATION:

APPLICANT: Gaiquer, Alexander

APPLICANT: Alqate, Paul A.

TITLE OF INVENTION: Mammalian

TITLE OF INVENTION: CEREALITERS ARE BETHES FOR THE DETECTION, DIAGNOSIS AND THER

FILE REFERENCE: 2077-001200

CURRENT APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

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PRIOR APPLICATION NUMBER: 60/200,545

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PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

db 25 SURASLETG 34

Search completed: January 2, 2003, 12:36:12  
Job time : 8.5 secs





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1 GENERAL INFORMATION:
2 APPLICANT: NAKAL, JUNGTHI
3 TITLE OF INVENTION: METHOD FOR PRODUCING A HUSBAND-PROTEIN CAPABLE OF REGULATING A
4 TITLE OF INVENTION: FLUORESCENCE PROPERTY OF GREEN FLUORESCENT PROTEIN, AND THE BUS
5 TITLE OF INVENTION: PRODUCED BY THE METHOD
6 FILE REFERENCE: 216,69236
7 CURRENT APPLICATION NUMBER: US/2000/05,047
8 PRIOR APPLICATION NUMBER: US/2000/05,047
9 PRIOR FILING DATE: 2000-11-22
10 NUMBER OF SEQ ID NOS: 17
11 SOFTWARE: Patent In Version 3.1
12 SEQ ID NO 1:
13 LENGTH: 21
14 TYPE: PRT
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Synthetic DNA
18 US 09 786 025A 6
19
20 Query Match: 60.0% Score 66; 146 24; Length 416;
21 Best Local Similarity: 76.2% Prod. No. 0.00046;
22 Matches: 15; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0;
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24 2 KRASLAGHAVAAGRESS 22
25 1 KRASLAGHAVAAGRESS 21
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1 NUMBER OF SEQ ID NOS: 15,005
2 SOFTWARE: Patent In Version 3.0
3 SEQ ID NO 31299
4 LENGTH: 604
5 TYPE: PRT
6 ORGANISM: Synthetic Construct
7 US 09 791 537 31299
8
9 Query Match: 60.0% Score 66; 108 21; Length 604;
10 Best Local Similarity: 76.9% Prod. No. 0.2;
11 Matches: 15; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;
12
13 4 KRASLAGHAVAAGRESS 22
14 1 KRASLAGHAVAAGRESS 207
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PCI-US96-1603-5
1 Sequence 5, Application PC/TUS9616603
2 GENERAL INFORMATION:
3 APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL CENTER
4 TITLE OF INVENTION: PHOTOSENSITIVE CYCLO MONOMER LIGANDS
5 NUMBER OF SEQUENCES: 9
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Fish & Richardson P.C.
8 STREET: 255 Franklin Street
9 CITY: Boston
10 STATE: MA
11 COUNTRY: USA
12 ZIP: 02110-2804
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent in Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: PT/US96/16603
20 FILING DATE: 15-OCT-1996
21 CLASSIFICATION:
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 08/542,927
24 FILING DATE: 13-OCT-1995
25 CLASSIFICATION:
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Fasse, J. Peter
28 REGISTRATION NUMBER: 42,043
29 REFERENCE/AGENT NUMBER: 6120/055W01
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 617/542-5070
32 TELEFAX: 617/542-8966
33 FAX: 200154
34 INFORMATION FOR SEQ ID NO: 5:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 20 amino acids
37 TYPE: amino acid
38 STRANEGNESS: not relevant
39 TOPOLOGY: both
40 MOLECULE TYPE: protein
41 PT-US96-1603-5
42 Query Match: 59.6%; Score 65; DB 1; Length 20
43 Best Local Similarity 79.9%; Prod. No. 0-0052;
44 Matches 15; Conservative 0; Mismatches 4; Indels
45
46
47 4 KKASLGTGHAVRAIGRLSS 22
48 11 1111111111111111
49 2 KKRWCKTGHAVRAIGRLSS 20
50
51
52 RESULT 11
53 PT-US96-08109-4
54 Sequence 4, Application PC/TUS9608109
55 GENERAL INFORMATION:
56 APPLICANT: University of Rochester
57 TITLE OF INVENTION: DETECTION BY FREY CHANGES OF LIGAND
58 TITLE OF INVENTION: BINDING BY GTP FUSION PROTEINS
59 NUMBER OF SEQUENCES: 33
60 CORRESPONDENCE ADDRESS:
61 ADDRESSEE: NIXON, HAPPAWE, DEVANS & FAYE LLP
62 STREET: Clinton Square, P.O. Box 1051
63 CITY: Rochester
64 STATE: New York
65 COUNTRY: USA
66 ZIP: 144604
67 COMPUTER READABLE FORM:
68 MEDIUM TYPE: Floppy disk
69 COMPUTER: IBM PC compatible
70 OPERATING SYSTEM: PC-DOS/MS-DOS
71 SOFTWARE: Patent in Release #1.0, Version #1.30
72 CURRENT APPLICATION DATA:

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1  APPLICATION NUMBER:  PCT/US98/08109
2  FILING DATE:
3  CLASSIFICATION:
4  PRIOR APPLICATION DATA:
5  APPLICATION NUMBER:  US 08/842,322
6  FILING DATE:  24-APR-1997
7  ATTORNEY/AGENT INFORMATION:
8  NAME:  Goldman, Michael L.
9  REGISTRATION NUMBER:  70,727
10  FILER'S CERT NUMBER:  176,60171
11  TELECOMMUNICATION INFORMATION:
12  TELEPHONE:  (716) 263-1304
13  TELEFAX:  (716) 263-1600
14  INFORMATION FOR SEQ ID NO:  4:
15  SEQUENCE CHARACTERISTICS:
16  LENGTH:  20 amino acids
17  TYPE:  amino acid
18  STRANDNESS:  not relevant
19  TOPOLOGY:  linear
20  MOLECULE TYPE:  peptide
21  PCT-US98-08109-4
22
23  Query Match      59.6%;  Score 65;  Length 20;
24  Best Local Similarity  79.4%;  Pred. No. 0.0052;
25  Matches  15;  Conservative  0;  Mismatches  4;  Indels
26
27  QY  4  PRACWORKCHAVEALGRLESS  22
28      11 11111111111111111111
29  DE  2  PRWORKCHAVEALGRLESS  20
30
31  RESULT 12
32  US-08-919-143-10
33  Sequence ID:  Application US/08919143
34  GENERAL INFORMATION:
35  APPLICANT:  Tsien, Roger Y.
36  APPLICANT:  Miyawaki, Atsushi
37  TITLE OF INVENTOR:  FLUORESCENT PROTEIN SENSORS FOR
38  TITLE OF INVENTOR:  DETECTION OF ANALYTES
39  NUMBER OF SEQUENCES:  56
40  CORRESPONDENCE ADDRESS:
41  ADDRESSEE:  Fish & Richardson P.C.
42  STREET:  4225 Executive Square, Suite 1400
43  CITY:  La Jolla
44  STATE:  CA
45  COUNTRY:  USA
46  ZIP:  92037
47  COMPUTER READABLE FORM:
48  MEDIUM TYPE:  Diskette
49  COMPUTER:  IBM Compatible
50  OPERATING SYSTEM:  Windows 95
51  SOFTWARE:  FastSeq for Windows Version 2.0b
52  CURRENT APPLICATION DATA:
53  APPLICATION NUMBER:  US/08/919,143
54  FILING DATE:
55  PRIOR APPLICATION DATA:
56  APPLICATION NUMBER:  05,818,252
57  FILING DATE:
58  ATTORNEY/AGENT INFORMATION:
59  NAME:  Haile, Ph.D., Lisa A.
60  REGISTRATION NUMBER:  38,447
61  POWERPC/PC-XT FTT NUMBER:  67,67,043001
62  TELECOMMUNICATION INFORMATION:
63  TELEPHONE:  619/678-5070
64  TELEFAX:  619/678-5099
65  INFORMATION FOR SEQ ID NO:  10:
66  SEQUENCE CHARACTERISTICS:
67  LENGTH:  20 amino acids
68  TYPE:  amino acid
69  TOPOLOGY:  linear
70  MOLECULE TYPE:  peptide
71  US-08-919-143-10

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1  APPLICATION NUMBER: 007506081010
2  FILING DATE:
3  CLASSIFICATION:
4  PRIORITY:
5  PRIOR APPLICATION DATA:
6  APPLICATION NUMBER: 00 02042 22
7  FILING DATE: 24-APR-1997
8  ATTORNEY/AGENT INFORMATION:
9  NAME: Goldman, Michael L.
10 REGISTRATION NUMBER: 90 27
11 TELEPHONE: 619 678 5099
12 TELETYPE: 619 678 5099
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: (716) 263-1304
15 TELEFAX: (716) 263-1600
16 INFORMATION FOR SEQ ID NO: 4:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 20 amino acids
19 TYPE: amino acid
20 STRANDNESS: not relevant
21 TOPOLOGY: linear
22 MOLECULE TYPE: peptide
23 PCT-US98-08109-4
24
25 Query Match 59.6% Score 65
26 best local similarity 78.4% Pred. No
27 Matches 15; Conservative 0; Mism
28
29 QY 4 PRACINOVAVPAICGLSS 22
30 11 11111111111111111111
31 DL 2 ERWQKCHAVPAICGLSS 20
32
33 RESULT 12
34 US-08-919-143-10
35 Sequence 10; Application US/08919143
36 GENERAL INFORMATION:
37 APPLICANT: Tsien, Roger Y.
38 APPLICANT: Miyawaki, Atsushi
39 TITLE OF INVENTION: FLUORESCENT PROTEIN
40 TITLE OF INVENTION: DETECTION OF ANAL
41 NUMBER OF SEQUENCES: 56
42 CORRESPONDENCE ADDRESS:
43 ADDRESSEE: Fish & Richardson P.C.
44 STREET: 4225 Executive Square, Sui
45 CITY: La Jolla
46 STATE: CA
47 COUNTRY: USA
48 ZIP: 92037
49 COMPUTER READABLE FORM:
50 MEDIUM TYPE: Diskette
51 OPERATING SYSTEM: Windows 95
52 SOFTWARE: FastSeq for Windows Vers
53 CURRENT APPLICATION DATA:
54 APPLICATION NUMBER: 00/0891919 143
55 FILING DATE:
56 PRIOR APPLICATION DATA:
57 APPLICATION NUMBER: 00 818 252
58 FILING DATE:
59 ATTORNEY/AGENT INFORMATION:
60 NAME: Haile, Ph.D.; Lisa A.
61 REGISTRATION NUMBER: 38 447
62 TELEPHONE: 619 678 5070
63 TELEFAX: 619 678 5099
64 INFORMATION FOR SEQ ID NO: 10:
65 SEQUENCE CHARACTERISTICS:
66 LENGTH: 20 amino acids
67 TYPE: amino acid
68 TOPOLOGY: linear
69 MOLECULE TYPE: peptide
70 US-08-919-143-10

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Query Match 59.6% Score 65; DB 13; Length 20;  
 Best Local Similarity 78.9%; Pred. No. 0.0052;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

27 4 PRASAD:GHAVRATIGLESS 22  
 11 | | | | | | | | | |  
 14 2 PRASAD:GHAVRATIGLESS 20  
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 RESULT 14  
 US-09-786-317-2  
 Sequence 26; Application US-09-786-317-2  
 GENERAL INFORMATION:  
 APPLICANT: Isobe, Yoshio Y.  
 APPLICANT: Baird, Geoffrey  
 TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS  
 FILE REFERENCE: 07/25/2001  
 CURRENT APPLICATION NUMBER: 09/09/016,920  
 CURRENT FILING DATE: 1999-05-21  
 NUMBER OF SEQ ID NOS: 63  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 26  
 LENGTH: 20  
 TYPE: PRT  
 ORGANISM: Melocoris allodapa  
 US-09-786-317-2

Query Match 59.6% Score 65; DB 17; Length 20;  
 Best Local Similarity 78.9%; Pred. No. 0.0052;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

27 4 PRASAD:GHAVRATIGLESS 22  
 11 | | | | | | | | | |  
 14 2 PRASAD:GHAVRATIGLESS 20  
 | | | | | | | | | |  
 RESULT 14  
 US-09-786-317-2  
 Sequence 26; Application US-09-786-317-2  
 GENERAL INFORMATION:  
 APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
 APPLICANT: Isobe, Yoshio Y.  
 APPLICANT: Baird, Geoffrey  
 TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS  
 FILE REFERENCE: PENDING  
 CURRENT APPLICATION NUMBER: 09/09/016,920  
 CURRENT FILING DATE: 1999-05-21  
 NUMBER OF SEQ ID NOS: 63  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 26  
 LENGTH: 20  
 TYPE: PRT  
 ORGANISM: Melocoris allodapa  
 US-09-786-317-2

Query Match 59.6% Score 65; DB 17; Length 20;  
 Best Local Similarity 78.9%; Pred. No. 0.0052;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

27 4 PRASAD:GHAVRATIGLESS 22  
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 14 2 PRASAD:GHAVRATIGLESS 20  
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 RESULT 14  
 US-09-786-317-2  
 Sequence 26; Application US-09-786-317-2  
 GENERAL INFORMATION:  
 APPLICANT: Isobe, Yoshio Y.  
 APPLICANT: Baird, Geoffrey  
 TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS  
 FILE REFERENCE: PENDING  
 CURRENT APPLICATION NUMBER: 09/09/016,920  
 CURRENT FILING DATE: 1999-05-21  
 NUMBER OF SEQ ID NOS: 63  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 26  
 LENGTH: 20  
 TYPE: PRT  
 ORGANISM: Melocoris allodapa  
 US-09-786-317-2

Query Match 59.6% Score 65; DB 19; Length 20;  
 Best Local Similarity 78.9%; Pred. No. 0.0052;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 27 4 PRASAD:GHAVRATIGLESS 22  
 11 | | | | | | | | | |  
 14 2 PRASAD:GHAVRATIGLESS 20  
 | | | | | | | | | |  
 Search completed: January 2, 2003, 14:56:22  
 Job time : 147 secs

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; NUMBER: 4; SEQ ID NOS: 29212
; SEQ ID NO: 1266
; LENGTH: 97
; TYPE: PRI
; ORGANISM: Propionis acnes
US-10-057-498-1266

Query Match
43.1%; Score 47; DB 6; Length 97;
Best local Similarity 42.1%; Pred. No. 13;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 TSLRRASLTGTHAVRAIG 19
DB 69 IKYRAATGSHSLSSVGR 87

RESULT 4
US-10-057-498-12775
; Sequence 12775, Application PC/TB5023.5727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatta, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shylan
; APPLICANT: Lodes, Michael
; APPLICANT: Bouison, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Bartick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 21021-5142
; CURRENT APPLICATION NUMBER: US/05/07-498
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 12775
; LENGTH: 427
; TYPE: PRI
; ORGANISM: Propionis acnes
US-10-057-498-12775

Query Match
43.1%; Score 47; DB 1; Length 627;
Best local Similarity 60.0%; Pred. No. 85;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 KRASLTGTHAVRAIG 18
DB 498 KRGLSPGHQVRAG 512

RESULT 4
US-10-057-498-12775
; Sequence 12775, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 21021-514
; CURRENT APPLICATION NUMBER: US/05/07-498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 12775
; LENGTH: 627
; TYPE: PRI
; ORGANISM: Propionis acnes
US-10-057-498-12775

Query Match
43.1%; Score 47; DB 6; Length 627;

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Best local Similarity 60.0%; Pred. No. 85;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 KRASLTGTHAVRAIG 18
DB 498 KRGLSPGHQVRAG 512

RESULT 5
US-09-724-676-82654
; Sequence 82654, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patent version 3.2
; SEQ ID NO 82654
; LENGTH: 136
; TYPE: PRI
; ORGANISM: Homo sapiens
US-09-724-676-82654

Query Match
40.8%; Score 44.5; DB 5; Length 136;
Best local Similarity 38.9%; Pred. No. 42;
Matches 14; Conservative 2; Mismatches 7; Indels 13; Gaps 1;

QY 1 TSLRRASLTG-----HAVAIGKLSST 24
DB 84 TSLVRAHLISGSIKLDYVKVSHVSALGKSMST 119

RESULT 6
US-09-724-676A-82654
; Sequence 82654, Application US/09/724,676A
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 82654
; LENGTH: 136
; TYPE: PRI
; ORGANISM: Homo sapiens
US-09-724-676A-82654

Query Match
40.8%; Score 44.5; DB 5; Length 136;
Best local Similarity 38.9%; Pred. No. 42;
Matches 14; Conservative 2; Mismatches 7; Indels 13; Gaps 1;

QY 1 TSLRRASLTG-----HAVAIGKLSST 24
DB 84 TSLVRAHLISGSIKLDYVKVSHVSALGKSMST 119

RESULT 7
US-09-724-676-82629
; Sequence 82629, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 82629
; LENGTH: 362

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TYPE: PPT  
ORGANISM: Homo sapiens  
US-09-724-676-82645

Query Match: 40.00% Score 44.5% ID %: Length 462;  
Best Local Similarity: 40.00% Prod. No. 1,1e-02;  
Matches 14; Conservative 2; Mismatches 7; Indels 13; Gaps 1;

27 1 ISLRVASTGTC - - - HAVVATGRSSST 23

111 11 11 11 11 11 11 11 11 11

DB 410 ISLVAVHLSGSIATKLYSKVRSBPVATGRSSST 44

RESULT 8

US-09-724-676-82645

Sequence 82645, Application US/0724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Comparison

CURRENT APPLICATION NUMBER: US/09724-676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patent In version 3.2

SEQ ID NO 82645

LENGTH: 462

TYPE: PPT

ORGANISM: Homo sapiens

US-09-724-676-82645

Query Match: 40.00% Score 44.5% ID %: Length 462;  
Best Local Similarity: 40.00% Prod. No. 1,1e-02;  
Matches 14; Conservative 2; Mismatches 7; Indels 13; Gaps 1;

27 1 ISLRVASTGTC - - - HAVVATGRSSST 23

111 11 11 11 11 11 11 11 11 11

DB 410 ISLVAVHLSGSIATKLYSKVRSBPVATGRSSST 44

RESULT 9

US-09-724-676A-82629

Sequence 82629, Application US/0724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Comparison

CURRENT APPLICATION NUMBER: US/09724-676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patent In version 3.2

SEQ ID NO 82629

LENGTH: 462

TYPE: PPT

ORGANISM: Homo sapiens

US-09-724-676A-82629

Query Match: 40.00% Score 44.5% ID %: Length 462;  
Best Local Similarity: 40.00% Prod. No. 1,1e-02;  
Matches 14; Conservative 2; Mismatches 7; Indels 13; Gaps 1;

27 1 ISLRVASTGTC - - - HAVVATGRSSST 23

111 11 11 11 11 11 11 11 11 11

DB 410 ISLVAVHLSGSIATKLYSKVRSBPVATGRSSST 44

RESULT 10

US-09-724-676A-82645

Sequence 82645, Application US/0724676A

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Comparison

CURRENT APPLICATION NUMBER: US/09724-676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patent In version 3.2

SEQ ID NO 82645

LENGTH: 462

TYPE: PPT

ORGANISM: Homo sapiens

US-09-724-676A-82645

Query Match: 40.00% Score 44.5% ID %: Length 462;  
Best Local Similarity: 40.00% Prod. No. 1,1e-02;  
Matches 14; Conservative 2; Mismatches 7; Indels 13; Gaps 1;

27 1 ISLRVASTGTC - - - HAVVATGRSSST 23

111 11 11 11 11 11 11 11 11 11

DB 410 ISLVAVHLSGSIATKLYSKVRSBPVATGRSSST 44

RESULT 11

US-09-724-676-82647

Sequence 82647, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Comparison

CURRENT APPLICATION NUMBER: US/09724-676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patent In version 3.2

SEQ ID NO 82647

LENGTH: 418

TYPE: PPT

ORGANISM: Homo sapiens

US-09-724-676-82647

Query Match: 40.00% Score 44.5% ID %: Length 418;  
Best Local Similarity: 40.00% Prod. No. 1,1e-02;  
Matches 14; Conservative 2; Mismatches 7; Indels 13; Gaps 1;

27 1 ISLRVASTGTC - - - HAVVATGRSSST 23

111 11 11 11 11 11 11 11 11 11

DB 406 ISLVAVHLSGSIATKLYSKVRSBPVATGRSSST 401

RESULT 12

US-09-724-676-82662

Sequence 82662, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Comparison

CURRENT APPLICATION NUMBER: US/09724-676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patent In version 3.2

SEQ ID NO 82662

LENGTH: 418

TYPE: PPT

ORGANISM: Homo sapiens

US-09-724-676-82662

Query Match: 40.00% Score 44.5% ID %: Length 418;  
Best Local Similarity: 40.00% Prod. No. 1,1e-02;  
Matches 14; Conservative 2; Mismatches 7; Indels 13; Gaps 1;

27 1 ISLRVASTGTC - - - HAVVATGRSSST 23

111 11 11 11 11 11 11 11 11 11

DB 406 ISLVAVHLSGSIATKLYSKVRSBPVATGRSSST 401

RESULT 13

US-09-724-676A-82667

Sequence 82667, Application US/09724676A













Thu Jan 2 14:11:11 2003

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27 4 PRASASLGHAVRATGRL 20
14 400 PRATASLGHAVRATGRL 419

PROSOL 14
10762
Probable amino acid decarboxylase - Streptomyces coelicolor
Submitted: 05 Nov 1999 #sequence revision of: Nov 1999 #text change 21-Jan-2000
Accession: U5762
P. Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.
Submitted to the EMBL data library, August 1999
Accession number: Z11588
Accession: U5762
Accession: preliminary; translated from Gly/EMBL/U488
Accession type: DNA
Accession: 1452 - SAG
Accession: references: EMBL:AL109742; F110N:YAB2074.1; GS0043:R00070; SC060R:SC7H2.31c
Accession: experimental source: strain A4(2)
Accession:
Accession: GS060R:SC7H2.31c
Accession: human glutamate decarboxylase

Query Match
Best Local Similarity 40.44; Score 44; DB 2; Length 452;
Matches 1; Conservation 2; Mismatches 4; Indels 4; Gaps 1;

27 2 SLPRASLGHAVRATGRL 20
14 400 AVERALLTTPAVTGPAPATGRL 423

PROSOL 15
375375
Reported local protein code: Salitobus solitarius
Submitted: 09 Oct 1997 #sequence revision 24 Oct 1997 #text change 17 Mar 1999
Accession: S75375
P. Saunders, D.W.; Kivok, D.C.; Smith, R.K.; Allard, G.; Chan, C.C.Y.; Liu, D.Y.; Penny, S.
Accession: 22:1763191, 1996
Accession: organizational characteristics and information content of an archaeal genome:
Accession number: S75375; M010:9705542; EMBL:8869719
Accession: S75375
Accession: multiple and sequence not shown; translation not shown
Accession type: DNA
Accession: 1458 - SUN
Accession: references: EMBL:Y9257; M010:17772; F110:29974; F110:1797780
Accession: experimental source: strain P2
Accession: The nucleotide sequence was submitted to the EMBL data library, September 1996

Query Match
Best Local Similarity 40.44; Score 44; DB 2; Length 458;
Matches 1; Conservation 2; Mismatches 5; Indels 0; Gaps 0;

27 2 SLPRASLGHAVRATGRL 20
14 400 SAKKSGTIVIAIKALGRL 474

Search completed: January 2, 2003, 14:29:16
Time: 05 secs

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Sequence version 5.1.1.4  
Copyright (c) 1993 - 2003 CompuLink Ltd.  
-M protein protein search, using SW model  
Run on: January 2, 2003, 12:26:31 : Search time 7 seconds  
(without alignments)  
136,279 entries in database  
Number of hits: 35 (76.41%)  
Post-processing: Minimum Match ok  
Maximum Match 100%  
Listing first 45 summaries  
Database: SwissProt 40.4  
Protein No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match %	Length	Id	Description
1	65	59.6	1006	1	KMUS_CHICK
2	58	53.2	448	1	KMUS_SHEEP
3	56	53.2	1147	1	KMUS_RABBIT
4	56	53.2	1176	1	KMUS_BOVINE
5	56	53.2	1514	1	KMUS_HUMAN
6	43	53.4	424	1	MAS_RAT
7	43	53.4	457	1	HELI_SLICER
8	42	49.5	700	1	HELI_SLICER
9	41.5	49.1	456	1	GLMO_RHET
10	41	47.6	437	1	HELI_SLICER
11	41	47.6	439	1	HELI_SLICER
12	41	47.6	664	1	ALOX_PITCAN
13	41	47.6	665	1	ALOX_PITCAN
14	41	47.6	1479	1	ALOX_PITCAN
15	41	47.6	1479	1	ALOX_PITCAN
16	40	46.7	466	1	HELI_SLICER
17	40	46.7	466	1	HELI_SLICER
18	40	46.7	466	1	HELI_SLICER
19	40	46.7	466	1	HELI_SLICER
20	40	46.7	466	1	HELI_SLICER
21	40	46.7	466	1	HELI_SLICER
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23	40	46.7	466	1	HELI_SLICER
24	40	46.7	466	1	HELI_SLICER
25	40	46.7	466	1	HELI_SLICER
26	40	46.7	466	1	HELI_SLICER
27	40	46.7	466	1	HELI_SLICER
28	40	46.7	466	1	HELI_SLICER
29	40	46.7	466	1	HELI_SLICER
30	40	46.7	466	1	HELI_SLICER
31	40	46.7	466	1	HELI_SLICER
32	40	46.7	466	1	HELI_SLICER
33	40	46.7	466	1	HELI_SLICER
34	40	46.7	466	1	HELI_SLICER
35	40	46.7	466	1	HELI_SLICER

Id	KMUS_CHICK	STANDARD	Prot	1000 AA
AC	P11799	P11799	1	1000 AA
BI	01-OCT-1989 (Rel. 12, Created)			
DI	01-OCT-1996 (Rel. 34, Last Sequence Update)			
FI	15 JUN 2002 (Rel. 41, Last Annotation Update)			
FE	Myosin light chain kinase, smooth muscle and non muscle isoforms			
DE	(EC 2.7.1.117) (MUSK) (Pentamer: Tetramer)			
OS	Gallus gallus (Chicken)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neornithae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus			
OX	NCBI TaxID 9031			
RN	[1]			
RP	SEQUENCE FROM N.A. (MUSK 210)			
RX	MEDLINE 9604976; PubMed 2604499			
RA	Watterson D.M., Gallus M., Lukes J., van Eliek L.L., Kinkor K.G.,			
RA	Stepanova O.V., Shrinisky V.P.			
RT	"Multiple gene products are produced from a novel protein kinase			
RT	transcription region."			
RL	FEBS Lett. 473:217-220(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A. (MUSK 100)			
RX	MEDLINE 9612792; PubMed 2151320			
RA	Olson N.J., Pearson R.H., Needleman P.S., Horwitz M.J., Kemp R.E.,			
RA	Means A.R.			
RT	"Regulatory and structural motifs of chickenizzard myosin light			
RT	chain kinase."			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:2284-2288(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A. (MUSK 100)			
RX	MEDLINE 9636174; PubMed 2292744			
RA	Shawaker M., Lee W., Chatterjee P., Kulkarni A.,			
RA	Mulligan P., Gupta Santos L., Wilson L., Lukes J.			
RT	"Use of DNA sequence and mutant analyses and antisense			
RT	oligonucleotides to examine the molecular basis of myosin			
RT	myosin light chain kinase autoinhibition, calmodulin recruitment, and			
RT	activity."			
RL	J. Cell Biol. 111:1107-1125(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A. (MUSK 100)			
RX	MEDLINE 9715758; PubMed 9030964			
RA	Guertler V., Jir, Russo M.A., Olson N.J., Lukes J.A., Means A.R.			
RT	"Regulatory and structural motifs of chickenizzard myosin light			
RT	chain kinase deduced from a cloned cDNA."			
RL	Biochemistry 25:8372-8381(1986).			
RN	[5]			
RP	SEQUENCE FROM N.A. (MUSK 100)			
RX	MEDLINE 9715758; PubMed 9030964			
RA	Guertler V., Jir, Russo M.A., Olson N.J., Lukes J.A., Means A.R.			
RT	"Regulatory and structural motifs of chickenizzard myosin light			
RT	chain kinase deduced from a cloned cDNA."			
RL	Biochemistry 25:8372-8381(1986).			
RN	[6]			
RP	SEQUENCE FROM N.A. (MUSK 100)			
RX	MEDLINE 9715758; PubMed 9030964			
RA	Guertler V., Jir, Russo M.A., Olson N.J., Lukes J.A., Means A.R.			
RT	"Regulatory and structural motifs of chickenizzard myosin light			
RT	chain kinase deduced from a cloned cDNA."			
RL	Biochemistry 25:8372-8381(1986).			
RN	[7]			
RP	SEQUENCE FROM N.A. (MUSK 100)			
RX	MEDLINE 9715758; PubMed 9030964			
RA	Guertler V., Jir, Russo M.A., Olson N.J., Lukes J.A., Means A.R.			
RT	"Regulatory and structural motifs of chickenizzard myosin light			
RT	chain kinase deduced from a cloned cDNA."			
RL	Biochemistry 25:8372-8381(1986).			
RN	[8]			
RP	SEQUENCE FROM N.A. (MUSK 100)			
RX	MEDLINE 9715758; PubMed 9030964			
RA	Guertler V., Jir, Russo M.A., Olson N.J., Lukes J.A., Means A.R.			
RT	"Regulatory and structural motifs of chickenizzard myosin light			
RT	chain kinase deduced from a cloned cDNA."			
RL	Biochemistry 25:8372-8381(1986).			
RN	[9]			
RP	SEQUENCE FROM N.A. (MUSK 100)			
RX	MEDLINE 9715758; PubMed 9030964			
RA	Guertler V., Jir, Russo M.A., Olson N.J., Lukes J.A., Means A.R.			
RT	"Regulatory and structural motifs of chickenizzard myosin light			
RT	chain kinase deduced from a cloned cDNA."			
RL	Biochemistry 25:8372-8381(1986).			
RN	[10]			
RP	SEQUENCE FROM N.A. (MUSK 100)			
RX	MEDLINE 9715758; PubMed 9030964			
RA	Guertler V., Jir, Russo M.A., Olson N.J., Lukes J.A., Means A.R.			
RT	"Regulatory and structural motifs of chickenizzard myosin light			
RT	chain kinase deduced from a cloned cDNA."			
RL	Biochemistry 25:8372-8381(1986).			

Arch. Biochem. Biophys. 299:242-247(1992).

SEQUENCE F 1765 1904 FROM N.A. (CE/KAIR).

MEETING 9224611; PubMed 1174915.

Collins M., Matrisian P.E., Elmer W.E., Shattuck R.L., Lukas T.L., van Eldik L.J., Waterson B.M.

"Structure and expression of a calcium-binding protein gene contained within a calmodulin-regulated protein kinase gene."

Mol. Cell. Biol. 12:2759-2771(1992).

FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A MYOSIN LIGHT CHAIN, WHICH LEADS TO THE FORMATION CALMODULIN/MYOSIN SIGNAL TRANSDUCTION COMPLEXES WHICH ALLOW SELECTIVE TRANSDUCTION OF CALCIUM SIGNALS.

FUNCTION: CATALYTIC ACTIVITY: ATP + [myosin light-chain] - ADP + [myosin light-chain] phosphate.

ALTERNATIVE PRODUCTS: At least 3 isoforms, MLCK-210/200 muscle form, MLCK-100/smooth muscle form and telokin; are produced by alternative initiation.

TISSUE SPECIFICITY: TELOKIN IS EXPRESSED IN SKELETON, HEART, LUNG, INTESTINE, AND SKELETAL MUSCLE ALTHOUGH THE LEVELS OF THE EXPRESSION IN THE LATTER BEING MUCH LESS THAN THAT IN THE GIZZARD.

DOMAIN: TELOKIN BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN LIKE C2 TYPE DOMAIN.

SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

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EMBL: X52876; CAA37056.1; -

EMBL: X52876; CAA37057.1; -

EMBL: X52876; CAA37058.1; -

EMBL: M11048; AAA49069.1; -

EMBL: M14953; AAA69664.1; -

EMBL: M46455; AAA49083.1; -

EMBL: M48284; AAA48647.1; -

EMBL: M48284; AAA53768.1; -

PIR: A25810; A25810.

PIR: A37099; A37099.

PIR: S11652; S11652.

BSSP: A56276; IILK.

InterPro: IPR000679; Euk\_Pkinase.

InterPro: IPR003961; FN\_III.

InterPro: IPR003006; Iq\_MHC.

InterPro: IPR003598; Iq\_C2.

InterPro: IPR004600; Iq\_Like.

InterPro: IPR002293; Ser\_Thr\_Pkinase.

Plant: PF00941; In3; 1.

Plant: PF00947; In3; 9.

Plant: PF00969; Pkinase; 1.

Prodom: P000060; Euk\_Pkinase; 1.

SMART: SM00360; FN3; 1.

SMART: SM00410; Iq\_Like; 1.

SMART: SM00408; Iq\_C2; 9.

SMART: SM00220; S\_IK; 1.

ProSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

ProSITE: PS00108; PROTEIN\_KINASE\_ST; 1.

ProSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.

Transferase Serine/threonine protein kinase; Calmodulin binding; ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat; Alternative initiation.

CHAIN 1 1906 MYOSIN LIGHT CHAIN KINASE, MLCK-210 (NON-MUSCLE ISOZYME).

CHAIN 945 1906 MYOSIN LIGHT CHAIN KINASE, MLCK 168 (SMOOTH-MUSCLE ISOZYME).

CHAIN 1750 1906 TELOKIN.

INIT\_MEI 945 945 FOR MECK 109.

INIT\_MEI 1750 1750 FOR TELOKIN.

FT DOMAIN 1346 1400 FIBRONECTIN TYPE-III.

FT DOMAIN 1453 1708 PROTEIN KINASE.

FT DOMAIN 1709 1904 IMMUNE C2 TYPE DOMAIN.

FT NP\_BIND 1459 1467 ATP (BY SIMILARITY).

FT BINDING 1482 1486 ATP (BY SIMILARITY).

FT ACT\_SITE 1574 1574 BY SIMILARITY.

FT DOMAIN 1716 1728 CALMODULIN AUTOINHIBITION (CARD) RESIDUE (POTENTIAL).

FT DOMAIN 1740 1749 CALMODULIN BINDING (POTENTIAL).

FT DOMAIN 1817 1833 MOTIF IA.

FT DOMAIN 1833 1833 MOTIF IB.

FT REPEAT 660 676 4 X REPEATS, MOTIF IIA.

FT REPEAT 758 774 IIA-1.

FT REPEAT 1107 1123 IIA-2.

FT REPEAT 1817 1833 IIA-3.

FT REPEAT 1833 1833 IIA-4.

FT REPEAT 693 708 IIB-1.

FT REPEAT 791 807 IIB-2.

FT REPEAT 1110 1156 IIB-3.

FT REPEAT 1281 1297 IIB-4.

FT REPEAT 1851 1866 IIB-5.

FT DOMAIN 970 1226 4 X REPEATS, MOTIF III.

FT REPEAT 970 987 III-1.

FT REPEAT 999 1016 III-2.

FT REPEAT 1061 1078 III-3.

FT REPEAT 1289 1296 III-4.

FT DOMAIN 1700 1763 CALMODULIN BINDING.

FT DOMAIN 1896 1906 POLY-GLU.

FT MOD\_RES 1748 1748 PHOSPHORYLATION.

FT M\_C\_2\_F\_3 1752 1752 PHOSPHORYLATION.

FT CONFLICT 1439 1439 R -> Q (IN REF. 4).

FT SEQUENCE 1906 AA; 210445 MW; A07D8A1B6FF3363 CAC64;

Query Match 59.6%; Score 65; DB 1; Length 1906;

Best Local Similarity 78.9%; Pred. No. 0.03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 REASLGTCGAVRATGRSS 22

DB 1731 RRGWKTCHAVRATGRSS 1749

RESULT 2

KMIS SHEEP

ID KMIS SHEEP STANDARD; PRI: 448 AA.

AC 002827;

DT 15-JUL-1998 (Ref. 36, Created)

DT 15-JUL-1998 (Ref. 36, Last sequence update)

DT 16 OCT 2001 (Ref. 40, Last annotation update)

LE Myosin light chain kinase, smooth muscle (M1752-1117) (MUSC)

DE [Contains: Telokin] (Fragment).

GN MYLK.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCPI\_134740 9940;

RN 111

RP SEQUENCE FROM N.A.

EX REGLINE 96174979; PubMed 8569750;

FA Pato M.D., Kore E., Lye S.J.

FT "phosphorylation and partial sequences of pregnant sheep myometrium myosin light chain kinase."

RL MOL. Cell. Biochem. 149:59-65(1995).

CC FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A MYOSIN LIGHT CHAIN.

CC CATALYTIC ACTIVITY: ATP + [myosin light chain] - ADP + [myosin light chain] phosphate.

CC DOMAIN: TELOKIN BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.



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FT ACT_SITE 817 817 BY SIMILARITY.
FI DOMAIN 1148 1147 POLY-GLU.
FI CONFLICT 1114 1114 C -> R (IN REF. 27).
SQ SEQUENCE 1147 AA: 125719 MW: 1039524CE31024 CRG64;

Query Match: 53.28; Score 58; DB 1; Length 1147;
Best local similarity: 73.79; Pred. No. 23;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0.

QY 4 PRASITICHAVAIRAGLESS 22
DB 974 RRKWKIGNAVAIRAGLESS 592

RESULT 4
KMUS_BOVIN
ID PRUS_BOVIN STANDARD; PRT: 1176 AA.
AC Q29924;
DI 15-JUL-1998 (Rel. 36, Created)
DI 15-JUL-1998 (Rel. 36, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin light chain kinase, smooth muscle (EE 2.7.1.117) (MLCK)
DE [Contains: telokin].
GN MYLK.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID 9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Stomach; PubMed:1294247;
RA Koyashiki H., Itoe A., Mikawa T., Kawayama H., Hotta Y., Masaki T.,
RI "Isolation of cDNA for bovine stomach 155 kDa protein exhibiting
RI myosin light chain kinase activity.";
PL J. Biochem. 112:786-791(1992).
QY 1- FUNCTION: CALCIUM/CAN-MEDIATED DEPENDENT FATTY ACID RESPONSIBLE FOR
QY SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE
QY IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC). AN EVENT THAT
QY FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS.
QY 1- CATALYTIC ACTIVITY: ATP + [myosin light chain] ADP + [myosin
QY light-chain] phosphate.
QY 1- SUBUNIT: TELOKIN BINDS CALMODULIN.
QY 1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS OF MLCK ARE PRODUCED BY
QY ALTERNATIVE INITIATION, A NON-MUSCLE FORM (WHICH IS THE LONGEST BY
QY FORM); A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SEQUENCE WITH
QY NO CATALYTIC ACTIVITY).
QY 1- SIMILARITY: BELONGS TO THE SEP/THE FAMILY OF PESTIN KINASES.
QY 1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
QY 1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
QY
QY This SWISS PROT entry is copyright. It is produced through a collaboration
QY between the Swiss Institute of Bioinformatics and the EMBL outstation -
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QY use by non-profit institutions as long as its content is in no way
QY modified and this statement is not removed. Usage by and for commercial
QY entities requires a license agreement (See http://www.isb-sib.ch/submit/
QY or send an email to license@isb-sib.ch)
QY
DB EMBL; S57131; AAR25704.1;
DB HSSP; P56276; 11LK.
DB InterPro: IPR000719; POK_pkinase
DB InterPro: IPR004561; FN_III.
DB InterPro: IPR004006; I4_MHC.
DB InterPro: IPR004598; I4_C2.
DB InterPro: IPR004530; I4_I1K1.
DB InterPro: IPR003390; Ser_Thr_Pkinase
DB Pfam: PF00041; 1n3; 1.
DB Pfam: PF00047; 1n; 2.
DB Pfam: PF00069; pkinase; 1.
DB ProDom: PD0000001; POK_pkinase; 1.

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DR SMART; SM00060; EN1; 1.
DR SMART; SM0413; C2_L1K1; 1.
DR SMART; SM0408; I032; 2.
DR SMART; SM00220; S_1K1; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_SF; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferring, Serine/threonine/tyrosine kinase; Calmodulin-binding;
KW ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
FT CHAIN 1 1176
FT MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT ISOZYME.
FT TELOKIN.
FT FOR TELOKIN.
FT DOMAIN 16 X 12 AA TALEM REPEATS.
FT REPEAT 1.
FT REPEAT 2.
FT REPEAT 3 (INCOMPLETE).
FT REPEAT 4.
FT REPEAT 5.
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FT REPEAT 11.
FT REPEAT 12.
FT REPEAT 13.
FT REPEAT 14.
FT REPEAT 15.
FT REPEAT 16.
FT FIBRONECTIN TYPE-III.
FT TELOKIN KINASE.
FT CALMODULIN BINDING.
FT C2-LIKE C2-TYPE DOMAIN.
FT ATP (BY SIMILARITY).
FT ATP (BY SIMILARITY).
FT BY SIMILARITY.
FT POLY-GLU.
FT SEQUENCE 1176 AA: 129821 MW: 1500054F42D4P97 CRG64;

Query Match: 53.28; Score 58; DB 1; Length 1176;
Best local similarity: 73.79; Pred. No. 24;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0.

QY 4 PRASITICHAVAIRAGLESS 22
DB 1003 RRKWKIGNAVAIRAGLESS 1021

RESULT 5
KMUS_HUMAN
ID KHL5_HUMAN STANFORD; PRT: 1214 AA.
AC Q15746; Q14844; Q16791; Q95796; Q95797; Q95798; Q95799; Q90HG5;
AC Q90HT9;
DI 15-JUL-1998 (Rel. 36, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Myosin light chain kinase, smooth muscle and non muscle isoforms
DE (EE 2.7.1.117) (MLCK) (isoform 1) (kinase related protein)
DE (KRP).
DE MYLK OR MLCK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
OX NCBI_TaxID 9606;
RN [1]
RP SEQUENCE FROM N.A. (1989M1).
RC Tissue: heart; isoform 1; non endothelial cells;
RC MEDLINE 9730446; PubMed 9160829;
RA Garcia J.G.N., Lazar V.L., Gilbert-McClain L.L., Gallacher P.J.,
RA Vorin A.D.;
RA "Myosin light chain kinase in endothelium: molecular cloning and

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171 regulation.";  
172 Am. J. Respir. Cell Mol. Biol. 16:489-494 (1997).  
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174 REVIEWS:  
175 Brinkov K.G., Garcia J.G.N.;  
176 Submitted (MAR 2002) to the EMBL/Genbank/DBM databases.  
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F1 PROPEP 17 134 POTENTIAL  
 F1 CHAIN 305 979 CATHESIN B LIKE CYSSTEINE PROTEINASE 6  
 F1 ACT SITE 133 133 BY SIMILARITY  
 F1 ACT SITE 305 979 BY SIMILARITY  
 F1 ACT SITE 425 425 BY SIMILARITY  
 F1 ACT SITE 118 118 BY SIMILARITY  
 F1 DISULFID 180 174 BY SIMILARITY  
 F1 DISULFID 166 233 BY SIMILARITY  
 F1 DISULFID 167 170 BY SIMILARITY  
 F1 DISULFID 203 237 BY SIMILARITY  
 F1 DISULFID 211 224 BY SIMILARITY  
 F1 CARBOHYD 196 196 N LINKED (GLUCNA... ) (POTENTIAL)  
 SQ SEQUENCE 479 AA: 42404 MW: 40873.6 E0619215F CR664  
 Query Match 47.4% Score 11; DB 1; Length 479;  
 Best Local Similarity 72.7% Prod. No. 47;  
 Matches 6; Conservative 1; Mismatches 0; Gaps 0  
 27 6 LERASTAGHVAIRIG 18  
 11 11111111  
 DB 601 LERASTAGHVAIRIG 311

RESULT 12  
 ALCOX PLVAN  
 ID ALCOX PLVAN STANDARD; PRT: 664 AA.  
 AC P04941;  
 D1 15 AUG 1997 (Rev. 05, Created)  
 D4 15 AUG 1997 (Rev. 05, Last sequence update)  
 D4 01 NOV 1997 (Rev. 05, Last annotation update)  
 DE Alcohol oxidase (EC 1.1.3.13) (WAX) (Metabolic oxidases (H-X)).  
 GN MOX.  
 OS Pichia anomala (Yeast) (Basidiomycota).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes;  
 OC Saccharomycetaceae; Saccharomyces; Pichia.  
 OX NCBI TaxID 4405;  
 RN 111  
 RP REGIERP FR R.A.  
 RX MEDLINE 65215671; PubMed 2982470;  
 RA Lebedev A.M., Eremeeva M., Vlasov G., Vasiljev G.L.,  
 R1 "Microbial alcohol and carbohydrate oxidases: an overview of the  
 oxidase in basidiomycota and characterization of a gene coding for methanol  
 oxidase in basidiomycota.";  
 R2 Nucleic Acids Res. 13: 4063-4062 (1985)  
 RN 121  
 RP SIMILARITY TO BACILLUS SUBSP. BACILLUS  
 RX MEDLINE 61104225; PubMed 2502169;  
 RA Carver J.P., Krasov P.  
 R1 "Inositol alcohol dehydrogenase and yeast alcohol oxidase are  
 homologous and share N-terminal homology with other flavoenzymes.";  
 R2 Mol. Biol. Evol. 6:144-150 (1991).  
 RN 131  
 RP REVIEW.  
 RX MEDLINE 91030674; PubMed 1882546;  
 RA van der Klei J.J., Harder W., Veenhuis M.  
 R1 "Biosynthesis and assembly of alcohol oxidase, a peroxisomal matrix  
 protein in methylotrophic yeasts: a review.";  
 R2 Yeast 7:195-209 (1991).  
 SC 1  
 SC 1 CATALYTIC ACTIVITY: A primary alcohol + O(2) -> an aldehyde +  
 H2O(2).  
 SC 1 COFACTOR: FAD.  
 SC 1 PATHWAY: IT IS THE FIRST REACTION IN C1 METABOLISM IN YEAST  
 WHEN FADH2 IS OXIDIZED TO FAD. FADH2, WHICH IS THE  
 BETWEEN LEWIS TO CARBON DIOXIDE.  
 SC 1 SUBUNIT: HOMOOLIGOMER.  
 SC 1 SUBCELLULAR LOCATION: Peroxisomal.  
 SC 1 SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY.  
 SC 1  
 SC 1 This SWISS Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation  
 at the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed, used by and for commercial  
 entities requires a license agreement (see <http://www.ebi.ac.uk/infocentre/licenses>).  
 SC 1 of Send an email to: license@ebi.ac.uk

CV or Send an email to: license@ebi.ac.uk.  
 DR EMBL: X02425; UAA26278.1;  
 DR EMBL: A11156; UAA00941.1;  
 DR PIR: A23010; OXHOAL;  
 DR 104010; UAA00941.1; 38% identical.  
 DR PIR: P00074; GM\* oxidase 1.  
 DR PROSITE: P00054; MICROOXIDASES; CTR: 1.  
 DR PROSITE: P00054; GM\* OXIDASE 1;  
 DR PROSITE: P00054; GM\* OXIDASE 2;  
 DR OXIDOREDUCTASE; Flavoprotein; FAD; Methanol oxidase (POTENTIAL).  
 F1 NP-610 8 574 574 FAD (ADP-FLAVO) (POTENTIAL).  
 F1 SITE 574 574 MICROOXIDASES; CTR: 1.  
 F1 SITE 664 664 MICROOXIDASES; CTR: 1.  
 SQ SEQUENCE 664 AA: 74089 MW: 64846.0 E06060000 CR664  
 Query Match 47.4% Score 11; DB 1; Length 664;  
 Best Local Similarity 47.4% Prod. No. 66;  
 Matches 6; Conservative 6; Mismatches 4; Gaps 0  
 27 4 LERASTAGHVAIRIG 18  
 11 11111111  
 DB 278 LERASTAGHVAIRIG 294  
 RESULT 13  
 PMA1 CANAL  
 ID PMA1 CANAL STANDARD; PRT: 695 AA.  
 AC P08877;  
 D1 01 DEC 1992 (Rev. 24, Created)  
 D4 01 DEC 1992 (Rev. 24, Last sequence update)  
 D4 16 OCT 2001 (Rev. 40, Last annotation update)  
 DE Plasma membrane ATPase 1 (P1-5.6.5.6) (Proton pump-1).  
 GN PMA1.  
 OS Candida albicans (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes;  
 OC Saccharomycetaceae; Saccharomyces; Candida.  
 OX NCBI TaxID 5476;  
 RN 111  
 RP SEQUENTIAL FROM R.A. AND PMA1 CANAL; CTR: 1.  
 RX MEDLINE 9291566; PubMed 1844644;  
 RA Mink B.C., Kurtz M.B., Martin J.A., Berlin D.S.  
 R1 "Cloning and characterization of the plasma membrane H(+)-ATPase from  
 Candida albicans.";  
 R2 J. Biol. Chem. 273:6826-6836 (1998).  
 RN 121  
 RP SEQUENTIAL FROM R.A. AND PMA1 CANAL; CTR: 1.  
 RX MEDLINE 9291566; PubMed 1844644;  
 RA Mink B.C., Kurtz M.B., Martin J.A., Berlin D.S.  
 R1 "Cloning and characterization of the plasma membrane H(+)-ATPase from  
 Candida albicans.";  
 R2 J. Biol. Chem. 273:6826-6836 (1998).  
 SC 1  
 SC 1 CATALYTIC ACTIVITY: ATP + H(2O) -> H(+) (H+) ADP + phosphate +  
 H(+) (H+).  
 SC 1 SUBCELLULAR LOCATION: Integral membrane protein.  
 SC 1 SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY  
 (E1-E2 ATPASES). SUBFAMILY 11A.  
 SC 1  
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 modified and this statement is not removed, used by and for commercial  
 entities requires a license agreement (see <http://www.ebi.ac.uk/infocentre/licenses>).  
 SC 1 of Send an email to: license@ebi.ac.uk  
 DR EMBL: M74075; AAA44319.1;  
 DR PIR: A11446; PCKP;  
 DR InterPro: IPR00157; ATPase\_E1\_F2.  
 DR InterPro: IPR004014; Cation\_ATPase.  
 DR InterPro: IPR000695; H\_ATPase.  
 DR InterPro: IPR001454; Kinase/hydrolase.  
 DR Pfam: PF00122; E1-E2\_ATPase; 1.  
 DR Pfam: PF00660; Cation\_ATPase\_N; 1.  
 DR Pfam: PF00660; Cation\_ATPase\_N; 1.  
 DR Pfam: PF00660; Cation\_ATPase\_N; 1.



1 SIMILARITY: BELONGS TO THE CALCIUM TRANSPORT ATPASES FAMILY (E1 E2  
ATPASES), SUBFAMILY IV.  
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3 between the Swiss Institute of Bioinformatics and the EMBL outstation  
4 at the European Bioinformatics Institute. There are no restrictions on its  
5 use by non-profit institutions as long as its content is in no way  
6 modified and this statement is not removed, usurped by and for commercial  
7 entities requires a license agreement (see <http://www.ebi.ac.uk/seqdb/doc/>  
8 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

EMBL: AB011368; BAB4/992.1;  
EMBL: AY029594; AAK33100.1; JOINED.  
EMBL: AY029487; AAK33100.1; JOINED.  
EMBL: AY029486; AAK33100.1; JOINED.  
EMBL: AY029489; AAK33100.1; JOINED.  
EMBL: AY029490; AAK33100.1; JOINED.  
EMBL: AY029491; AAK33100.1; JOINED.  
EMBL: AY029492; AAK33100.1; JOINED.  
EMBL: AY029493; AAK33100.1; JOINED.  
EMBL: AY029494; AAK33100.1; JOINED.  
EMBL: AY029495; AAK33100.1; JOINED.  
EMBL: AY029496; AAK33100.1; JOINED.  
EMBL: AY029497; AAK33100.1; JOINED.  
EMBL: AY029498; AAK33100.1; JOINED.  
EMBL: AY029499; AAK33100.1; JOINED.  
EMBL: AY029500; AAK33100.1; JOINED.  
EMBL: AY029501; AAK33100.1; JOINED.  
EMBL: AY029502; AAK33100.1; JOINED.  
EMBL: AY029503; AAK33100.1; JOINED.  
EMBL: AB011148; BAAZ4942.1;  
Genbank: BBN11647; AIP1nc.  
MIM: 605805;  
MIM: 105840;

InterPro: IPR001757; ATPase E1 E2.  
InterPro: IPR00154; H+ATPase.  
Pfam: Pfam002; Hydrolase 1.  
Pfam: Pfam119; CALATPASE.  
Pfam: Pfam154; ATPase E1 E2 1.  
K0 Hydrolases; Transmembrane; Phosphorylation; Manganese; ATP binding;  
K0 Multi-pass family.

E1	DOMAIN	1	95	CYTOPLASMIC (POTENTIAL).
E1	TRANSMEM	67	106	POTENTIAL.
E1	DOMAIN	107	110	EXTRACELLULAR (POTENTIAL).
E1	TRANSMEM	111	128	POTENTIAL.
E1	DOMAIN	129	979	CYTOPLASMIC (POTENTIAL).
E1	TRANSMEM	411	422	POTENTIAL.
E1	DOMAIN	437	462	EXTRACELLULAR (POTENTIAL).
E1	TRANSMEM	463	484	POTENTIAL.
E1	DOMAIN	485	1087	CYTOPLASMIC (POTENTIAL).
E1	TRANSMEM	1088	1198	POTENTIAL.
E1	DOMAIN	1199	1119	EXTRACELLULAR (POTENTIAL).
E1	TRANSMEM	1120	1140	POTENTIAL.
E1	DOMAIN	1141	1170	CYTOPLASMIC (POTENTIAL).
E1	TRANSMEM	1171	1192	POTENTIAL.
E1	DOMAIN	1193	1199	EXTRACELLULAR (POTENTIAL).
E1	TRANSMEM	1200	1222	POTENTIAL.
E1	DOMAIN	1223	1228	CYTOPLASMIC (POTENTIAL).
E1	TRANSMEM	1229	1249	POTENTIAL.
E1	DOMAIN	1250	1267	EXTRACELLULAR (POTENTIAL).
E1	TRANSMEM	1268	1292	POTENTIAL.
E1	DOMAIN	1293	1499	CYTOPLASMIC (POTENTIAL).
E1	TRANSMEM	1500	427	EXTRACELLULAR (POTENTIAL).
E1	DOMAIN	1041	1041	MAGNESIUM (BY SIMILARITY).
E1	METAL	1045	1045	MAGNESIUM (BY SIMILARITY).
E1	DOMAIN	447	470	POLY GLY.
E1	CONFLICT	488	488	C - R (IN REF. 5).
52	SEQUENCE	1499	AA: 147687 MW: 14996400.65A686 CRE94;	

Query Match  
Best local similarity 40.0%; Score 41; Pos 1; Length 1499;  
Matches H: Conservation 6; Mismatches 7; Indels 0; Gaps 0;

QY 4 REASLATCHAVARAJARAJESHI 24  
31 JUL 2003 11:11:11  
DB 480 QRCSTGSHSVKVVHRTQST 499  
Search completed: January 2, 2003, 12:29:08  
Job time: 9 secs

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IR SMART: SM00060; FN3; 1.
IR SMART: SM00220; S_LIK; 1.
IR PROSITE: PS00107; TYRK; 1.
IR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
IR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW AIP binding; Transferrase.
SQ SEQUENCE 732 AA; 80617 MW; 78671701E174AUF CPC64.

Query Match 45.0%; Score 49; DB 5; Length 732;
Best Local Similarity 45.0%; Pred. No. 31;
Matches 9; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 LRRASLTGCHAVRAICRLSS 22
    ||| ||| ||| ||| |||
DB 429 LRRKWKTCGNATRALGGMAN 448

RESULT 8
Q9V7G6 PRELIMINARY; PRT; 786 AA.
DI 01-MAR-2001 (FEBRELL 16, Created)
DI 01-JUN-2002 (FEBRELL 16, Last sequence update)
DE Strachin-Mack (Fragment).
GN STEN-MACK OR A225 OR C28304 OR C018255.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Phylodoidea; Neuroptera; Ephemeroptera; Diptera; Brachycera; Muscomorpha;
OC Phylodoidea; Neuroptera; Ephemeroptera; Diptera; Brachycera; Muscomorpha;
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN ORIGIN:
EX MEDLINE 97218468; PubMed 9147992;
KA Kojima S., Mishima M., Mabeuchi I., Botta Y.;
PT A single Drosophila melanogaster myosin light chain kinase gene
RT produces multiple isoforms whose activities are differently
    regulated.*;
RL Genes Cells 1:855-871(1996).
RC 1. SIMILARITY: BELONGS TO THE SH3/THE FAMILY OF PROTEIN KINASES.
DR FMBP; 09965; BAA20906.1; -.
DR BSSP; Q63450; IA06.
DR FlyBase: FB00013988; Strn-Mck.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003961; FN_L11.
DR InterPro: IPR003599; Ia.
DR InterPro: IPR003006; Ia_MHC.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00041; In3; 1.
DR Pfam: PF00047; Ia; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_Pkinase; 1.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00220; S_LIK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_AIP; UNKN_WN_1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Alternative splicing; Myosin; Serine/threonine-protein kinase.
FT NON_TER 1
FT NON_TER 842
SQ SEQUENCE 842 AA; 91899 MW; 17483006E5E8A0C CPC64;

Query Match 45.0%; Score 49; DB 5; Length 842;
Best Local Similarity 45.0%; Pred. No. 36;
Matches 9; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 3 LRRASLTGCHAVRAICRLSS 22
    ||| ||| ||| ||| |||
DB 657 LRRKWKTCGNATRALGGMAN 676

RESULT 10
Q9V7G6 PRELIMINARY; PRT; 913 AA.
DI 01-MAY-2000 (FEBRELL 13, Created)
DI 01-MAY-2000 (FEBRELL 13, Last sequence update)
DI 01-JUN-2002 (FEBRELL 21, Last annotation update)
DE Strn-Mck protein.
GN STEN-MACK OR C28304 OR C018255.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Phylodoidea; Neuroptera; Ephemeroptera; Diptera; Brachycera; Muscomorpha;
OC Phylodoidea; Neuroptera; Ephemeroptera; Diptera; Brachycera; Muscomorpha;
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN ORIGIN:
EX MEDLINE 20511811; PubMed 10991296;
KA Champagne M.B., Edwards P.A., Erickson H.L., Richard D.F.;
PT "Drosophila strachin-Mck is a novel member of the strachin-Mck myosin light
    chain kinase family.*"
KA J. Mol. Biol. 300:759-777(2000).
DR FMBP; A255670; AAC01797.1; -.
DR BSSP; Q63450; IA06.
DR FlyBase: FB00013988; Strn-Mck.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003961; FN_L11.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00041; In3; 1.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_Pkinase; 1.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00220; S_LIK; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_AIP; UNKNOWN_1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
FT NON_TER 1
FT NON_TER 913
SQ SEQUENCE 784 AA; 86183 MW; F0512925A02AB259 CPC64;

Query Match 45.0%; Score 49; DB 5; Length 786;
Best Local Similarity 45.0%; Pred. No. 34;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRRASLTGCHAVRAICRLSS 22
    ||| ||| ||| ||| |||
DB 440 LRRKWKTCGNATRALGGMAN 449

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DB EMBL: AF004596; AAF04596.1;  
DB EMBL: AF004592; AAF04592.1;  
KW Hypothetical protein; complete; full-length;  
SQ SEQUENCE: 597 AA; 62491 MW; 9f965367306a42f0 CRC64;

Query Match: 43.1%; Score 47; DB 16; Length 597;  
Best Local Similarity: 66.7%; Prod. No. 62;  
Matches: 1; Unsubstantive: 0; Mismatches: 5; Indels: 0; Gaps: 0;

27 5 ASLCTCHAVPAIGPL 20  
3 1 1 1 1 1 1 1 1 1  
14 429 AAGGAGHVVSNIGPL 443

Search completed: January 2, 2003, 12:40:46.  
Job time: 27.5 secs

